

FIGURE 1

CGGACGCGTGGGTGCGAGGCGAAGGTGACCGGGGACCGAGCATTTCAGATCTGCTCGGTAGA
 CCTGGTGCACCACCACC**ATG**TTGGCTGCAAGGCTGGTGTGTCTCCGGACACTACCTTCTAGG
 GTTTTCCACCCAGCTTTCCACCAAGGCCCTCCCTGTTGTGAAGAAATCCATCACGAAGAATCA
 ATGGCTGTTAACACCTAGCAGGGAATATGCCACCAAAAACAAGAAATGGGATCCGGCGTGGGA
 GAACCTGGCCAAAGAACTCAAAGAGGCAGCATTGGAACCATCGATGGAAAAAATATTTAAAT
 GATCAGATGGGAAGATGGTTGTTGCTGGAGGGGCTGCTGTTGGTCTTGGAGCATTGTGCTA
 CTATGGCTTGGGACTGTCTAATGAGATTGGAGCTATTGAAAAGGCTGTAATTTGGCCTCAGT
 ATGTCAAGGATAGAATTCAATCCACCTATATGTACTTAGCAGGGAGTATTGGTTTAAACAGCT
 TTGTCTGCCATAGCAATCAGCAGAACGCCCTGTTCTCATGAACCTCATGATGAGAGGCTCTTG
 GGTGACAATTGGTGTGACCTTTGCAGCCATGGTTGGAGCTGGAATGCTGGTACGATCAATAC
 CATATGACCAGAGCCCAGGCCCAAAGCATCTTGCTTGGTTGCTACATTCTGGTGTGATGGGT
 GCAGTGGTGGCTCCTCTGACAAATATTAGGGGGCTCCTCTCTCATCAGAGCTGCATGGTACAC
 AGCTGGCATTGTGGGAGGCCCTCTCCACTGTGGCCATGTGTGCGCCCACTGAAAAGTTTCTGA
 ACATGGGTGCACCCTGGGAGTGGGCCCTGGGTCTCGTCTTTGTGTCTCATTTGGGATCTATG
 TTTCTTCCACCTACCACCGTGGCTGGTGCCACTCTTTACTCAGTGGCAATGTACGGTGGATT
 AGTTCTTTTTCAGCATGTTCTCTGTATGATACCCAGAAAGTAATCAAGCGTGCAGAAGTAT
 CACCAATGTATGGAGTTCAAAAATATGATCCATTAACTCGATGCTGAGTATCTACATGGAT
 ACATTTAAATATATTATGCGAGTTGCAACTATGCTGGCACTGGAGGCAACAGAAAAGAA**AG**
AGGTGACTCAGCTTCTGGCTTCTCTGCTACATCAAAATATCTGTTTAAATGGGGCAGATATGC
 ATTAATAATGTTGTACAAGCAGCTTTCGTTGAAGTTTAGAAGATAAGAAACATGTCATCATA
 TTTAAATGTTCCGGTAATGTGATGCCTCAGGTCTGCCCTTTTCTTGAGAAATAAATGCAGT
 AATCCTCTCCCAATAAGCACACACATTTTCAATTTCTCATGTTTGAGTGATTTTAAATGTT
 TTGGTGAATGTGAAAACATAAAGTTTGTGTGATGAGAATGTAAGTCTTTTTTCTACTTTAAAA
 TTTAGTAGGTTCACTGAGTAACATAAAATTTAGCAAACTGTGTTTGACATATTTTTTGGAGT
 GCAGAATATTGTAATTAATGTCATAAGTGATTGGAGCTTTGGTAAAGGACACAGAGAGAAG
 GAGTCACCTGCAGTCTTTTGTTTTTTTAAATACTTAGAAGCTTAGCACTTGTGTTATTGATT
 GTGAGGAGCCAGTAAGAAACATCTGGGTATTGGAACAAGTGGTCATTGTTACATTCAATTT
 GCTGAACCTTAAACAAACCTGTTTCATCTGAAACAGGCACAGTGATGCATTCTCTGCTGTTG
 CTTCTCAGTGCTCTCTTTCCAATATAGATGTGGTCATGTTGACTTTGTACAGAATGTTAATC
 ATACAGAGAATCCTTGATGGAATTATATATGTGTGTTTTTACTTTTGAATGTTTACAAAAGGAA
 ATAACCTTTAAACATATTCTCAAGAGAAAATATTCAAAGCATGAAATATGTTGCTTTTTCCAG
 AATAACAAACGTATACTCATG

104117.040660

FIGURE 2

MLAARLVCLRTLPSRVFHPAFTKASPVVKNSITKNQWLLTPSREYATKTRIGIRRGRTGOEL
KEAALEPSMEKIFKIDQMGRWFVAGGAAVGLGALCYGLGLSNEIGAIEKAVIWPQYVKDRI
HSTYMYLAGSIGLTALSAIAISRTPVLMNFMMRGSWVTIGVTFAMVAGAGMLVRSIPYDQSP
GPKHLAWLLHSGVMGAVVAPLTLGGPLLIRAAWYTAGIVGGLSTVAMCAPSEKFLNMGAPL
GVGLGLVFVSSSLGSMFLPPTTVAGATLYSVAMYGGLVLFMFLLYDTQKVIKRAEVSPMYGV
QKYDPINSMLSIYMDTLNIFMRVATMLATGGNRKK

0990440.11401

FIGURE 3

GAAGGCTGCCTCGCTGGTCCGAATTCCGGTGGCGCCACGTCGCCCGCGTCTCCGCGCTTCTGCAT
 CGCGGCTTCGCGCGCTTCCACCTAGACACCTAACAGTCGCGGAGCGCGCGCGCTGTCGAGGG
 GGTCCGCACGGGGAGTCGGGCGGTCTTGTGCATCTTGGCTACCTGTGGGTTCGAAGTGCAGTGC
 ACATCCGAGACTGGTTCAGGAGCATCCCGCGCATCAGCGCGTATTGGTTCGCCCGCCACCGCT
 CGCGTCCGCTTGGTTCGGCAAACTCGCGCTCATCAGCCCGCGCTACCTCTTCCCTTCGGCCCGGA
 AGCCTTCCTTTATCGCTTTTCAGATTGGAGGCCAATCACTGCCACCTTTTATTTCCCTGTGGT
 TCCAGGAACCTGGATTCTTTTATTTGGTCAATTTATATTTCTTATATCAGTATTCTACGGCA
 CTTGAAACAGGAGCTTTTGATGGGAGGCCAGCAGACTATTTATTATGCTCCTCTTTAACTG
 TGTCAGTACTTTATGCTCGGGCCAGCTGAACAGAGACATGATTGTATCATTTTGGTTTGGGA
 ACACGATTTAAGGCTGCTATTACCTGGGTTATCCTTGGATTCAACTATATCATCGGAGG
 CTCGGTAAATCAATGAGCTTATTGGAATCTGGTTGGACATCTTTATTTTTCTTAATGTTCA
 GATACCCAAATGGACTTGGGAGGAAGAAATTTTCTATCCACACCTCAGTTTTTGTACCGCTGG
 CTGCCAGTAGGAGGAGGAGATCAGGATTTGGTGTGCCCGCTGCTAGCATGAGGCGAGC
 TGCTGATCAGAATGGCGGAGCGGAGACACAACCTGGGCGCAGGGCTTTCGACTTGGAGACC
 ACTGAAGGGGCGGCGCTCGGGCAGCGCTCCTCTCAAGCCACATTTCTCCAGTGCTGGGTG
 CACTTAAACAACCTGCTTCTGGCTAACACTGTGGACCTGACCCACACTGAATGTAGTCTTTT
 AGTACAGAGACAAGTTCTTTAAATCCCGAAGAAAAATATAAGTGTTCACAAGTTTCCACGAT
 TCTCAATTCAAGTCCTTACTGCTGTGAAGAACAATACCAACTGTGCAAAATGGAACCTGAC
 TACATTTTGGGTGCTCTCTCTCTCTCCCTTTCCGCTGAATAATGGGTTTTAGCGGGTCTCT
 AATCTGCTGCGCATTTGAGCTGGGCTGGGTCAACAAACCTTCCCAAAAGGACCTTATCTCTT
 TCTTGCACACATGCTCTCTCCCACTTTTCCCAACCCCCACATTTGCAACTAGAAAAAGTTG
 CCCATAAAATTTGCTCTGCGCTTGACAGGTTCTGTTATTTATTGACTTTTGGCAAGGCTGGTC
 ACAACAATCATATTACGTTTATTTCCCTTTTGGTGGCAGAACTGTTACCAATAGGGGGAG
 AAGACAGGCCAGCATTTCTCAGCTTTTGGAAATGCTTGCAGTACATCCGTTGTT
 AACCGTTTGGCCACTCTTCAGATATTTTTTATAAAAAAGTACCACCTGAGTTCATGAGGGCCA
 CAGATTGGTTATTAATGAGATACGAGGTTGGTCTGGGTGTTTGTTCCTGAGCTAAGTGA
 TCAGACTGTAGTGGAGTTCAGCTAACATGGGTTAGGTTTAAACCATGGGGGATGCACCCC
 TTTGCGTTTCATATGTAGCCCTACTGGCTTTGTGAGCTGGAGTAGTTGGGTTGCTTTGTGT
 TAGGAGGATCCAGATCATGTTGGCTACAGGAGAGATGCTCTCTTTGAGAGGTCCTGGGCATTG
 ATTCCCATTTCAATCTCATTTGGATATGTGTTTATTGAGTAAAGGAGGAGACCCCTCATA
 CGGTATTTAAATGTCACTTTTTGCCTATCCCCCGTTTTTGGTCAATGTTTCAATTAATTTG
 GAGGAAGGCCGAGCTCCTCTCTGCAGTAGATCATTTTTTAAAGCTAATGTAAGCAGCATCTA
 AGGGAATAACATGATTAAAGTTGAATGGCTTAGAATCATTTGGGTTTGGGGTGTGTTA
 TTTTGAGTCATGAATGTACAAGCTCTGTGAATCAGACCGCTTAAATACCCACACCTTTTTT
 TCGTAGTGGGCTTTTCTATCAGAGCTTGGCTCATAACCAAAATAAAGTTTTTGAAGGCCA
 TGGCTTTTTCACACAGTTTATTTTATTTATGACGTTATCTGAAAGCAGACTGTTAGGAGCAGT
 ATTGAGTGGCTGTACACACTTTGAGGCAACTAAAAAGGCTTCAAAACGTTTGTATCAGTTTCTT
 TCTCAGGAACATTGTGCTTAACAGTATGACTATTTCTTCCCCACTCTTAAACAGTGTGAT
 GTGTGTTATCCTAGGAAATGAGAGTTGGCAACAACTTCTCAATTTGAATAGAGTTTGTGTG
 TACTTCTCCATTAATTTATATGATAAAATAGTGGGGAGAGTCTGAACCTTCACTGTGA
 TGTTTTGTGTTTCTCTGCGCCACAATAAAGTTTACTTGAATAATTTAGAGGCCATTACT
 CCAATTTGTTGCAGTACACTCATTGTACAGCGGTGGAGACTCATTTGTATGTATAAGAAATA
 TTTCTGACAGTGAGTGAGCCCGGAGTCTCTGGTGTACCCCTCTTACAGCTAGCTGCCTGCGAG
 CAGTCATTTTTTCTTAAGCGTTTACAAGTATTTAGAAGTTTTAGTTCAGGGCAAAATGTTT
 ATGAAGTTTATTCCTCTTAAACATGGTTAGGAAGCTGTAGACGTATTGATTTTGTCTGGATT
 ATGTTTCTGGAATAATTTTACAAAACAGCTATTTAGTTTGTGATGACAAAGGCCAAACA
 TGACAGTGGATTCTCTTTACAAATGAAAAAAAATCCTTATTTTGTATAAAGGACTTCCC
 TTTTTGTAAACTAATCCTTTTATTGTAATAAATGTAAATTAATGTGCACTTG

FIGURE 4

MSDIGDWFRSIPAITRYWFAATVAVPLVGKLGGLISPAYLFLWPEAFLYRFQIWRPITATFYF
PVGPGTGFLYLVLNLYFLYQYSTRLETGAFDGRPADYLFMLLFNWICIVITGLAMDMQLLMIP
LIMSVLYVWAQLNRDMIVSFWFGTRFKACYLPWVILGFNYIIGGSVINELIGNLVGHLYFFL
MFRYPMDLGGRNFLSTPQFLYRWLPSRRGGVSGFGVPPASMRRAADQNGGGGRHNWQGGRFL
GDQ

Transmembrane domain:

amino acids 98-116, 152-172

N-myristoylation site.

amino acids 89-95, 168-174, 176-182, 215-221, 221-227, 237-243

Glycosaminoglycan attachment site.

amino acids 218-222

GGGGCCGCGGTCTAGGGCGGCTACGTGTGTTGCCATAGCGACCAATTTGCATTAACTGGTGT
GTAGCTTCTATCCTGGGGGCTGAGCGACTGCGGGCCAGCTCTTCCCTACTCCCTCTCGGCT
CCTTGTGGCCCAAAGGCTAACCGGGGTCGCGCGGTCTGGCCTAGGGATCTTCCCGTTGCC
CCTTTGGGCGGG**CATG**GCTGCGGAAGAAGAAGACGAGGTGGAGTGGGTAGTGGAGAGCATCT
CGGGGTTCTGCGAGGCCCAGACTGGTCCATCCCCATCTTGGACTTTGTGGAACAGAAATGT
GAAGTTAACTGCAAAGGAGGGCATGTGATAACTCCAGGAAGCCAGAGCCGGTGATTTTGGT
GGCCTGTGTTCCCTTGTTTTGATGATGAAGAAGAAAGCAAATTGACCTATACAGAGATT
ATCAGGAATACAAAGAACTAGTTGAAAAGCTGTTAGAAGGTTACCTCAAAGAAATTGGAAT
AATGAAGATCAATTTCAAGAAGCATGCACCTTCTCCTCTTGCAAAGAGCCATACATCACAGG
CATTTTGCAACCTGTGTTGGCAGCAGAAATTTTACTATCTTTAAAGCAATGATGGTCCAGA
AAAA**CATTGAAATGCAGCTGCAAGCCATT**CGAATAATTCAAGAGAGAAATGGTGTATTACCT
GACTGCTTAA**CCGATGGCTCTGATGTGGT**CAGTGACCTTGAACACGAAGAGATGAAA**TCCT**
GAGGGAA**GTCTTAGAAAA**TCAAAGAGGAATATGACCAGGAAGAAGAAAGGAAGAGGAAAA
AACAGTTATCAGAGGCTAA**ACAGAA**GAGCCACAGTGCA**TTCCAGTGAAGT**GCAATAATG
ATAAT**TCCCAAGGGGATGGTGAACATTTTG**CACACCCAC**CTCAGAAGTTAAAT**GCATT
TGCTAATCAGTCAATAGAA**CTTTG**GGAAGAAAAGTGGAAAG**GTCTGAAACTT**CTCCCTCC
CACAAAAGG**CTGAAGAT**CCTGGCTTAGAGCATCGAGCA**TTGAAGCA**CAATAGCA**AA**
TTATCAGTACTTGGAA**CAGAAGAACTTC**GGCAACGAGAAC**CATCTATG**CAAGCAGAAAGAGA
TAAGTTAGTGTCCATGAGAAAGGATATGAGGACT**TAACAGATACAA**ATATGGAGCAGAAAG
GAAA**CCCATCTGGG**GAGTAGAGGAAATGACAGAGAA**ACCAGAA**ATGACAGCAGAGGAGAA**G**
CAAACATTACTAAAGAGGAGATTGCTTG**CAGAGAA**ACTCAAAGAAAG**ATTATTA**TAAG**TA**
ATAATTAAGAACATTTAACAAATGGAAGTTCAAAT**TGCTTAAAA**ATAAATTATTTAGT**C**
CTTACACTG

FIGURE 6

MAAEEDEVEVWVESIAGFLRGPDWSIPIILDFVEQKCEVNCKGGHVITPGSPEPVILVACVP
LVFDDEEESKLTYTEIHQEYKELVEKLLEGYLKEIGINEDQFQEACTSPLAKTHTSQAILQP
VLAAEDFTIFKAMMVQKNIEMLQAIIRIIQERNGLVLPDCLTDGSDVVSLEHEEMKILREVL
RKSKEEYDQEEERKRKKQLSEAKTEEPTVHSSEAAIMNNSQGDGEHFAHPPSEVKMHFANQS
IEPLGRKVERSETSSLPQKGLKIPGLEHASIEGPANLSVLGTEELRQREHYLKQKRDKLMS
MRKDMRTKQIQNMEQKGKPTGEVEEMTEKPEMTAEKQTLKRRLLAEKLKEEVINK

N-glycosylation sites.

amino acids 224-228, 246-250, 285-289

N-myristoylation site.

amino acids 273-279

Amidation site.

amino acids 252-256

Cytosolic fatty-acid binding proteins.

amino acids 78-108

GGGCACAGCACATGTGAAGTTTTTGATGATGAAGAAGAAAGCAAATTGACCTATACAGAGAT
TCATCAGGAATACAAAGAACTAGTTGAAAAGCTGTTAGAAGGTTACCTCAAAGAAATTGGAA
TTAATGAAGATCAATTTCAAGAGCATGCACCTTCCTCTTGCAAGACCCATACATCACAG
GCCATTTTTGCAACCTGTGTTGGCAGCAGAAGATTTTACTATCTTTAAAGCAATGATGGTCC
AGAAAAACATGAAATGCAGCTGCAAGCCATTCGAATAATCAAGAGCAAAATGGTGTATTA
CCTGACTGCTTAAACCGATGGCTGTGTGTCGATGACCTTGAACACGAAGATGAAAT
CTTGAGGGGAAGTTCTTAGAAATCAAAGAGGAATGATGACCGGAA

FIGURE 8

GCGTGGTTTTTGTCTGCAATAGGCGGCTTAGAGGGAGGGGCTTTTCGCCCTATACCTACTG
 TAGCTTCTCCACGTATGGACCTTAAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTG
 TCTCAGCTCTAGGATGTCGCTTCTCCACTAGAAGCTCTTCTGAGGGAGGTAATAAAAAAC
 AGTGGAAATGGAAGAAACAGTGTCTGTAGTCATCCTGTAATATGCTCCTGTCAACAATGTATAC
 ATTCTGCTAGGTGCCATATTCTTCTTAAAGCTCAAGTCGCATCTTACTAGTGAAGTATT
 CTGCCAATGAAGAAAAACAGTATGATTATCTTCCAACCTACTGTGAATGTGTGCTCAGAAGCTG
 GTGAAGCTAGTTTTCTGTGTGCTTGTGCATTCTGTGTATATAAGAAAGATCATCAAAGTAG
 AAATTTGAAATATGCTTCTGGAAGGAATCTCTGATTTCATGAAGTGGTCCATTCTCGCT
 TTCTTTATTTCTCGGATAACTTGATTGTCTTCTATGTCCTGTCCATCTTCAACCGCCATG
 GCTGTTATCTTCTCAAATTTTAGCATTATAACAACAGCTCTTCTATTCAAGGATAGTGCTGAA
 GAGGCGTCTAAACTGGATCCAGTGGGCTTCCCTCCTGACTTTATTTTTGTCTATTGTGGCT
 TGACTGCCGGGACTAAAACTTTACAGCACAACTTGGCAGGACGTGGATTTTCATCACAGATGCC
 TTTTTCAGCCCTTCCAATTTCTGCTTCTTTTCAGAAGTGAGTGTCCAGAAAAGACAATTG
 TACAGCAAAAGGAATGGACTTTTCTGGAAGCTAAATGGAACACCACAGCCAGAGTTTTTCAGTC
 ACATCCGCTTGTGGCATGGGCCATGTTCTTATTATAGTCCAGTGTTTTATTCTTCAATGGCT
 AATATCTATAATGAAAGATACTGAAGGAGGGGAACACAGCTCAGTGAAGCATCTTTCATACA
 GAACAGCAAACCTCTATTTCTTGGCATTCTGTTTAAATGGGCTGACTCTGGGCCCTCAGAGGA
 GTAACCGTGATCAGATTAAAGACTGTGGATTTTTTTATGGCCACAGTGATTTTCAGTAGCC
 CTATTTTTTTGAAGTGCATTCAGGGCCCTTTCAGTGGCTTTTCATTCTGAAGTTCCTGGATA
 CATGTTCCATGCTCTGTGATGGCCAGGTTACCACTGTGCATTATCACACAGTGTCTCTGG
 TCTTTGACTTCAGGCCCTTCCCTGGAATTTTTCTTGGAGCCCCACTCAGTCTCTCTCTATA
 TTTATTATTAATGCGCAGCAAGCCTCAAGTTCGGAATACGCCACCTAGGCAAGAAAGGATCG
 AGATCTAAGTGGCAATCTTGGGAGCGTTCAGTGGGGATGGAGAAGAACTAGAAAGACTTA
 CCAAACCAAGAGTGATGAGTCAGATGAAGATACTTTCTAACTGGTACCACCATAGTTTGGCA
 GCTCTCTGAACCTTATTTTACATTTTCAGTGTTTGAATATTTATCTTTTCACTTTTGATA
 AACCAGAAATGTTTTCTAAATCCTAATATTCTTGCATATATCTAGCTACTCCCTAAATGGTT
 CCATCCAAGGCTTAGAGTACCAAGGCTAAGAAATCTAAGAACTGATACAGGAGTAACA
 ATATGAAGAATTCATTAATATCTCAGTACTGTATAATCAGAAAGTTATATGTGCAGATTAT
 TTTCTTGGCCCTTCAAGCTTCCAAAAAAGCTTGAATAATCATGTTAGCTATAGCTTGTATAT
 ACACATAGAGATCAATTTGCCAAATATTACAATCATGTAGTCTCAGTTTACATGCCAAAGT
 TTTCCCTTTTAAACATTATAAAGCTAGGTGTCTCTGAAATTTTGGGCCCTAGAGATAGT
 CATTTTGAAGATTAAGAGCAACGGGACCCTTTCTAAAAACGTTGGTTGAAGGACCTAAATAC
 CTGGCCATACCATAGATTTTGGGATGATGTAGTCTGTGCTAAATATTTTGTGAAGAAGCAGT
 TTCTCAGACACAACATCTCAGAATTTTAATTTTTAGAAATTCATGGGAAATTTGGATTTTTGT
 AATAATCTTTTGTATTTTTAAACATTTGGTTCCTTAGTCACCATAGTTACCACTTGTATTTTA
 AGTCATTCTTAAACAAGCGGTGGGCTTTTTTCTCCTCAGTTTGGGAGAAAAATCTTGAT
 GTCAATCTCCTGAATTATTACATTTTGGAGAATAAGAGGGCACTTTTATTATTAGTTACT
 AATTCAAGCTGTGACTATTGTATATCTTTCCAAGAGTTGAATGTCTGGCTTCAAGTATAC
 CAGATTGTCAAGCTGATGCTTAGGAACCTTTTAAAGGGATCCTTTCAAAGGATCACT
 AGCAAAACACATGTTGACTTTTAACTGATGTATGAATATTAATACTCTAAAAATAGAAAGAC
 AGTAATATATAAGTCACTTTTACAGTGCTACTTCACTTAAAGTGCAGTGGTATTTTTTCATG
 GTATTTTGCATGCAGCCAGTTAACTCTCGTAGATAGAGAAGTCAGGTGATAGATGATATTA
 AAATTAAGCAAAACAGTACTGTCTCAGGGTCATGCAGCTGGGTGATGATAGAAGAGTGG
 CTTTAACTGGCAGGCTGTATGTTTACAGACTACCATCTGTAATATGAGCTTTATGGTGT
 CATTTCTCAGAAATATATACATTTCTGCTCTCCTTTCTCCTAAGTTTCATGCAGATGAATATA
 AGGTAATATACTATTATATAATTTCAATTTGTGATATCCCAATAATATGACTGGCAAGAAATG
 GTGGAATTTTGAATTTAAATAATTATTAAACCT

FIGURE 9

MEKQCCSHPVICLSLSTMYTFLFGAIFIALSSSRILLVKYSANEENKYDYLPTTVNVCSELVK
LVFCVLVSFCVIKKDHQSRNLKYASWKEFSDFMKWSIPAFLYFLDNLI VFVLSYLQPMAMAV
IFSNFSIIT TALLFRIVLKRRLNWIQWASLLTFLSIVALTAGTKTLQHNLAGRGFHHDAFF
SPSNSCLLFRSECPKRDNCTAKEWTFPEAKWNNTARVFSHIRLGMGHVLIIVQCFISSMANI
YNEKILKEGNQLTESIFIQNSKFLYFYGILFNLTLGLQRNSRNDQIKNCGFYGHSAFSAVALI
FVTAFOQLSVAFILFLDNMFMHVLMAQVTTIITVLSVLDFRPSLEFFLEAPSVLLSIFI
YNASKPQVSEYAPROERIRDLSGNLWERSSGDGEELERLTKPKSDESDEDTF

Transmembrane domains:

amino acids 16-36 (type II), 50-74, 147-168, 229-250, 271-293,
298-318, 328-368

N-glycosylation sites.

amino acids 128-132, 204-208, 218-222, 374-378

Glycosaminoglycan attachment site.

amino acids 402-406

N-myristoylation sites.

amino acids 257-263, 275-281, 280-286, 284-290, 317-323

FIGURE 10

CGTGCCTGCGCAATGGGTGTCGGGTCCGCTTTTTCCCAATCCGGACGTAATCGTGGTTTTTG
TTCTGCAATAGGCGGCTTAGAGGGAGGGGCTTTTTCGCCTATACCTACTGTAGCTTCTCCAC
GTATGGACCCTAAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTGTCTCAGCTCTAG
GATGTGCGTTCTTCCACTAGAAGCTCTTCTGAGGGAGGTAATTA AAAACAGTGGAATGGAA
AAACAGTGCTGTAGTCATCCTGTAATATGCTCCTTGTCAACAATGTATACATTCTGCTAGG
TGCCATATTCATTGCTTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATTCTGCCAATGAAG
AAAACAAGTATGATTATCTTCCAAC TACTGTGAATGTGTGCTCAGAACTGGTGAAGCTAGTT
TTCTGTGTGCTTGTGTCATTCTGTGTTATAAAGAAAGATCATCAAAGTAGAAATTTGAAATA
TGCTTCCTGGAAGGAATTCTCTGATTT CATGAAGTGGTCCATTCTGCCTTTCTTTATTTCC
TGGATAACTTGATTGTCTTCTATGTCCTGTCCTATCTTCAACCAGCCATGGCTGTTATCTTC
TCAAATTTTAGCATTATAACAACAGCTCTTCTATT CAGGATAGTGTGAAGAGGCGCTAAAA
CTGGATCCAGTGGGCTTCCCTCCTGACTTTATTTTTGTCTATTGTGGCCTTACTGCCGGGA
CTAAAACTTTA

FIGURE 11

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGGCCGGCTTGGCTAGCGCGCGGGCGGCC
 GTGGCTAAGGCTGCTACGAAGCGAGCTTGGGAGGAGCAGCGGCCTGCGGGGCAGAGGAGCAT
 CCCGCTACCAAGTCCCAAGCGGCGTGGCCCCGCGGGTCATGGCCAAAGGAGAAGGCCGCCGAG
 AGCGGCTCCGCGGCGGGGCTGCTACCCACAGCATCCTCCAAGCACTGAACGCCCGGGCCCA
 GGTGAAGAAAGAACCGAAAAAGAAACAACAGTTGCTGTTTTGCAACAAGCTTTGCTATG
 CACTTGGGGGAGCCCCCTACCAAGTGACGGGCTGTGCCCTGGTTCTTCTCTCAGATCTAC
 CTATTGGATGTGGCTCAGGTGGGCCCTTTCTGCTGCCATCATCCTGTTTGTGGGCCGAGC
 CTGGGATGCCATCAGACCCCTGTTGGGCTCTGCATCAGCAAATCCCCCTGGACCTGCC
 TGGGTCGCCCTTATGCCCTGGATCATCTTCCACGCCCTGGCCGTCAATGGCTACTTCCCT
 ATCTGGTTGCTGCCGACTTCCACACGGCCAGACCTATTGGTACCTGCTTTTCTATTGCCT
 CTTTGAACAATGGTCAGGTGTTTCCATGTTCCCTACTCGGCTCTCACCATGTTTCATCAGCA
 ACCGAGCAGACTGAGCGGGATTCTGCCACCGCCTATCGGATGACTGTGGAAGTGCTGGGCAC
 AGTGCTGGGCACGGCGATCCAGGGACAACCTGTTGGGCCAAGCAGACACGCCTTGTTCACAG
 ACTTCAATAGCTCTACAGTAGCTTCACAAAGTGCCAAACATACACATGGCACCACTTCACAC
 AGGGAACGCAAAAGGCATACCTGCTGGCAGCGGGGTCATTGTCTGTATCTATATAATCTG
 TGCTGTCTATCCTGATCCTGGGCGTGCAGGAGCAGAGAGAACCCTATGAAGCCAGCAGTCTG
 AGCCAATCGCCTACTTCCGGGGCTACGGCTGGTCATGAGCCACGGCCCATACATCAAACCT
 ATTACTGGCTTCTCTTACCTCCTTGGCTTTTATGCTGGTGGAGGGGAACCTTTGTCTGTT
 TTGCACCTACACCTTGGGCTTCCGCAATGAATCCAGAATCTACTCCTGGCCATCATGCTCT
 CGGCCACTTTAACCATTCCTATCTGGCAGTGGTTCTTGACCCGTTTGGCAAGAGACAGCT
 GTATATGTTGGGATCTCATCAGCAGTGCCATTTCTCATCTTGGTGGCCCTCATGGAGAGTAA
 CCTCATCTATTACATATGCGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCTTCTTAC
 TACCCTGGTCCATGCTGCCTGATGTCATTGACGACTTCCATCTGAAGCAGCCCCACTTCCAT
 GGAACCGAGCCCATCTTCTTCTCTTCTATGTCTTCTCACCAGATTGTGCTCTGGAGTGTCTC
 ACTGGGCATTCTACCTCAGTCTGGACTTTGCAGGGTACCAGACCCGTGGCTGCTCGCAGC
 CGGAACGTGTCAAGTTTACTGAACATGCTCGTGACCATGGCTCCCATAGTTTCTCATCCTG
 CTGGGCCCTGCTGCTCTTCAAATGTACCCCATTTGATGAGGAGAGGCGGCGGCAAGATAAGAA
 GGCCCTGCAGGCACTGAGGGACGAGGCCAGCAGCTCTGGCTGCTCAGAAACAGACTCCACAG
 AGCTGGCTAGCATCCTCTAGGGCCGCCACGTTGCCGAAGCCACCATGCAGAAGGCCACAG
 AAGGGATCAGGACCTGTCTGCCGGCTTGCTGAGCAGCTGGACTGTCAGGTGCTAGGAAGGGAA
 CTGAAGACTCAAGAGGTTGGCCAGGACACTTGCTGTGCTCACTGTGGGGCCGGCTGCTCTG
 TGGCCTCCTGCTCCCTCTGCCTGCTGTGGGGCCAAGCCTGGGGCTGCCACTGTGAATA
 TGCCAAGCACTGATCGGGCTAGCCGGAACACTAATGTAGAAACCTTTTTTTACAGAGCC
 TAATTAATACTTAATGACTGTGTACATAGCAATGTGTGTATGTATATGTCTGTGAGCTA
 TTAATGTTATTAATTTTCATAAAGCTGGAAGC

FIGURE 12

MWLRWALS LPPSSCLWAE PGMPSQTPWWASASANPPGPAWVALCPGSSSRPWPSPSLPTSSSG
SCPTSH TARPIGT CFSIASLKQWSRVSMFPTRLSPCSSATEQTERDSATAYRMTVEVLGTVL
GTAIQGQIVGQADTPCFQDFNSSTVASQSANHTHGTTSHRETQKAYLLAAGVIVCIYIICAV
ILILGVREQREP YEAQQSEPIAYFRGLRLVMSHGPYIKLITGFLFTSLAFMLVEGNFVL FCT
YTLGFRNEFQNL LLAIMLSATLTIPWQWFLTRFGKKTAVYVGISSAVPFLILVALMESNLI
ITYAVAVAAGISVAAAFLLPWSMLPDVIDDFHLKQPHFGTEPIFFSFYVFFTKFASGVSLG
ISTLSLDFAGYQTRGCSQPERVKFTLNMLVTMAPIVLILLG LLLFKMYPIDEERRRQNK KAL
QALRDEASSSGCSETDSTELASIL

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FIGURE 13

GGGAAACGCAAAGGCATACCTGCTGGCAGCGGGGGTCATTGTCTGTATCTATATAATCTGT
GCTGTCATCCTGATCCTGGGCGTGCGGGAGCAGAGAGAACCCTATGAAGCCCAGCAGTCTGA
GCCAATCGCCTACTTCCGGGGCCTACGGCTGGTCATGAGCCACGGCCCATACATCAAACCTTA
TTACTGGCTTCCTCTTCACCTCCTTGGCTTTTCATGCTGGTGGAGGGGAACCTTGTCTTGTTT
TGCACCTACACCTTGGGCTTCCGCAATGAATTCCAGAATCTACTCCTGGCCATCATGCTCTC
GGCCACTTTAACCATTCCCATCTGGCAGTGGTTCTTGACCCGGTTTGGCAAGAAGACAGCTG
TATATGTTGGGATCTCATCAGCAGTGCCATTTCTCATCTTGGTGGCCCTCATGGAGAGTAAC
CTCATCATTACATATGCGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCTTCTTACT
ACCCTGGTCCATGCTGCCTGATGTATTGACGACTTCCATCTGAAGCAGCCCCACTTCCATG
GAACCGAGCCCAT

00000000 11111111

FIGURE 14

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGGATTTACAAAAGGTGCAGGT
 ATGAGCAGGTCTGAAGACTAACATTTTGTGAAGTTGTAAACAGAAAACCTGTTAGAAATGT
 GGTGGTTTCAGCAAGGCCTCAGTTTCCTTCCTTCAGCCCTTTGTAATTTGGACATCTGCTGCT
 TTCATATTTTCATACATTACTGCAGTAACACTCCACCATATAGACCCGGCTTTACCTTATAT
 CAGTGACACTGGTACAGTAGCTCCAGAAAAATGCTTATTTGGGGCAATGCTAAATATTGCGG
 CAGTTTTATGCATTGCTACCATTTATGTTTCGTTATAAGCAAGTTCATGCTCTGAGTCCTGAA
 GAGAACGTTATCATCAAATTAACAAGGCTGGCCTTGTAAGTGAATACTGAGTTGTTTAGG
 ACTTTCTATTGTGGCAAACCTCCAGAAAAACAACCCTTTTGTGTCACATGTAAGTGGAGCTG
 TGCTTACCTTTGGTATGGGCTCATTATATATGTTTGTTCAGACCATCCTTTCCTACCAAATG
 CAGCCCAAAATCCATGGCAAACAAGTCTTCTGGATCAGACTGTTGTTGGTTATCTGGTGTGG
 AGTAAGTGCACCTTAGCATGCTGACTTGCTCATCAGTTTTCAGCAGTGGCAATTTTGGGACTG
 ATTTAGAACAGAACTCCATTGGAACCCGAGGACAAAGGTTATGTGCTTCACATGATCACT
 ACTGCAGCAGAATGGTCTATGTCATTTTCCTTCTTTGGTTTTTTCCTGACTTACATTCGTGA
 TTTTCAGAAAATTTCTTTACGGGTGGAAGCCAATTTACATGGATTAACCTCTATGACACTG
 CACCTTGCCCTATTAACAATGAACGAACACGGCTACTTTCAGAGATATTTGATGAAAGGAT
 AAAATATTTCTGTAATGATTATGATTCTCAGGGATTGGGGAAAGGTTACAGAAGTTGCTTA
 TTCTTCTCTGAAATTTCAACCACTTAATCAAGGCTGACAGTAACACTGATGAATGCTGATA
 ATCAGGAAACATGAAAGAAGCCATTTGATAGATTATTTCTAAAGGATATCATCAAGAAGACTA
 TTAAAAACACCTATGCCTATACTTTTTATCTCAGAAAATAAAGTCAAAGACTATG

MWWFQQGLSFLPSALVIWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNI
 AAVLCIATIYVRYKQVHALSPEENVIKLNKAGLVGLISCLGLSVANFQKTTTFAAHVSG
 AVLTFGMGSLYMFVQTILSYQMOPKIHGKQVFWIRLLLVICGVSAKLSMLTCSVLHSGNF
 TDLEQKLHWNPEDKGYVLHMITTAEWSMSFSFFGFLLTYIRDFQKISLRVEANLHGLTLYD
 TAPCPINNRETRLLSRI

FIGURE 16

CGGACGCTTGGGCNGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGTGCCTGATGCCGAGT
TCCGTCTCTCGGGTCTTTTCCCTGGTCCCAGGCCAAAGCGGAGCGGAGATCCTCAAACGGCCTA
GTGCTTCGCGCTTCCGGAGAAAATCAGCGGTCTAATTAATTCCTCTGGTTTGTGAAGCAGT
TACCAAGAATCTTCAACCCTTTCCACAAAAGCTAATTGAGTACACGTTCCCTGTTGAGTACA
CGTTCTGTGATTACAAAAGGTGCAGGTATGAGCAGGTCTGAAGACTAACATTTTGTGAA
GTTGTAAACAGAAAACCTGTTAGAAATGTGGTGGTTTCAGCAAGGCCTCAGTTTCCTTCCT
TCAGCCCTTGTAATTTGGACATCTGCTGCTTTCATATTTTCATACATTACTGCAGTAACACT
CCACCATATAGACCCGGCTTTACCTTATATCAGTGACACTGGTACAGTANC

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FIGURE 17

CCCACGCGTCCGCCCGCGCTGCGTCCCGGAGTGCAAGTGAGCTTCTCGGCTGCCCCGCGGG
 CCGGGGTGCGGAGCGCAGATCGCGCCGCTTCTCGGCCTCCTTCTGGTCTTCGCCGGCTGCAC
 CTTGCGCTTGTAATTGCTGTCGACGCGACTGCCCGCGGGCGGAGACTGGGCTCCACCGAGG
 AGGCTGGAGGCAGGTGCGTGTGGTTCCCTCCGACCTGGCAGAGCTGCGGGAGCTCTCTGAG
 GTCCTTCGAGAGTACCGGAAGGAGCACCAGGCCTACGTGTTCTGTCTTCTGCGGCGCCTA
 CCTCTACAAACAGGGCTTTGCCATCCCCGGCTCCAGCTTCTGAATGTTTTAGCTGGTGCCT
 TGTTTGGGCCATGGCTGGGGCTTCTGCTGTGCTGTGTGTGACCTCGGTGGGTGCCACATGC
 TGCTACCTGCTCTCCAGTATTTTGGCAAACAGTTGGTGGTGTCTACTTTCCTGATAAAGT
 GGCCCTGCTGCAGAGAAAGGTGGAGGAGAACAGAAACAGCTTGTTTTTTTTCTTATTGTTTT
 TGAGACTTTTCCCCATGACACCAAAGTGGTCTTGAACCTCTCGGCCCAATTCTGAACATT
 CCCATCGTGCAGTTCTTCTTCTCAGTTCTTATCGGTTTGATCCCATATAATTTTATCTGTGT
 GCAGACAGGGTCCATCCTGTCAACCCTAACCTCTCTGGATGCTCTTTTCTCCTGGGACACTG
 TCTTTAAGCTGTTGGCCATTGCCATGGTGGCATTAAATCCTGGAACCCCTATTAAAAAATTT
 AGTCAGAAACATCTGCAATTGAATGAAACAAGTACTGCTAATCATATACAGTAGAAAAGA
 CACATGATCTGGATTTTCTGTTTGCCACATCCCTGGACTCAGTTGCTTATTTGTGTAATGGA
 TGTGGTCCCTCTAAAGCCCCCTATTGTTTTGATTGCCTTCTATAGGTGATGTGGACACTGTG
 CATCAATGTGCAGTGTCTTTTCAGAAAGGACACTCTGCTCTTGAAGGTGTATTACATCAGGT
 TTTCAAACAGCCCTGGTGTAGCAGACACTGCAACAGATGCCTCCTAGAAAATGCTGTTTGT
 GGCCGGGC CGGTGGCTCAGCCTGTAATCCAGCACTTTGGGAGGCCGAGGCCGGTGATTCT
 ACAAGGTGAGGAGTTCAAGACCAGCCTGGCCAAGATGGTGAAATCCTGTCTCTAATAAAAAAT
 ACAAAAATTAGCCAGGCGTGGTGGCAGGCACCTGTAATCCAGCTACTCGGGAGGCTGAGGC
 AGGAGAATTGCTGAACCAAGGTGGCAGAGGTTGCAGTAAGCCAAGATCACACCACTGCACT
 CCAGCCTGGGTGATAGAGTGAGACACTGTCTTGAC

FIGURE 18

MRPLLGLLLVFAGCTFALYLLSTRLPGRRLGSTEEAGGRSLWFPSDLAE LRELSEVLREYR
KEHQAYVFLFLFCGAYLYKQGFAIPGSSFLNVLAGALFGPWLGLLLCCVLT SVGATCCYLLSS
IFGKQLVVSYPDPKVALLQRKVEENRNSLFFFLFLRLFPMT PNWFLNLSAPILNIPIVQFF
FSVLIGLIPYNFICVQTSILSTLTSLDALFSWDTVFKLLAIAMVALIPGTLIKKFSQKHLQ
LNETSTANHIHSRKDT

Important features:**Signal peptide:**

amino acids 1-17

Transmembrane domains:

amino acids 101-123, 189-211

N-glycosylation sites.

amino acids 172-176, 250-254

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 240-244, 261-265

N-myristoylation site.

amino acids 13-19, 104-110, 115-121, 204-210

Amidation site.

amino acids 27-31

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 4-15

Protein splicing proteins.

amino acids 25-31

Sugar transport proteins.

amino acids 162-172

FIGURE 19

CCGAGGCGGGAGGAGCCCCGAGGGGCGCGAGCCCCGCATGAATCATTGTAGTCAATCATTTT
 CCAGTTCTCAGCCGCTCAGTTGTGATCAAGGGACACGTGGTTTCCGAAGTGCCAGCTCAGAA
 TAGGAAAATAACTTGGGATTTTATATTGGAAGACATGGATCTTGCTGCCAACGAGATCAGCA
 TTATGACAACTTTTACAGAGACTGTTGATTGGTGAGACAGACCGGCCATCAGTGTGGCATG
 TCAGAGAAGGCAATTGAAAAATTTATCAGACAGCTGCTGGAAGAATGAACCTCAGAGACC
 CCCCCGCAGTATCCTCTCCTTATAGTTGTGTATAAGGTTCTCGCAACCTTGGGATTAATCT
 TGCTCACTGCCTACTTTGTGATTCAACCTTTAGCCCCATTAGCACCTGAGCCAGTGCCTTCT
 GGAGCTCACACCTGGCGCTCACTCATCCATCACATTAGGCTGATGTCCTTGCCCATTGCCAA
 GAAGTACATGTCAGAAAATAAGGGAGTTCCTCTGCATGGGGTGATGAAGACAGACCCCTTTC
 CAGACTTTGACCCCTGGTGGACAAACGACTGTGAGCAGAATGAGTCAGAGCCCATTCCTGCC
 AACTGCACTGGCTGTGCCAGAAACACCTGAAGGTGATGCTCCTGGAAGACGCCCCAAGGAA
 ATTTGAGAGGCTCCATCCACTGGTATCAAGACGGGAAAGCCCTGTTGGAGGAAGAGATTC
 AGCATTTTTTGTGCCAGTACCCTGAGGCGACAGAAGGCTTCTGTAAGGGTTTTTCGCCAAG
 TGGTGGCGCTGCTTTCCTGAGCGGTGGTCCCATTTCTTATCCATGGAGGAGACCTCTGAA
 CAGATCACAAATGTTACGTGAGCTTTTTCTGTTTTCACTCACCTGCCATTTCCAAAAGATG
 CCTCTTTAAACAAGTGCTCCTTTCTTACCCAGAACCTGTTGTGGGGAGTAAGATGCATAAG
 ATGCCTGACCTATTTATCATTGGCAGCGGTGAGGCCATGTTGCAGCTCATCCCTCCCTTCCA
 GTGCCGAAGACATTGTGAGTCTGTGGCCATGCCAATAGAGCCAGGGGATATCGGCTATGTGG
 ACACCAACCCACTGGAAGGTCTACGTTATAGCCAGAGGGGTCCAGCCTTTGGTCATCTGCGAT
 GGAACCGCTTTCTCAGAAGCTAGAGGAAATAGAACTGTGCACAGGAACAGCTTCCAGAGCCGA
 AAACCAGGTTGAAAGGGGAAAAATAAAAACAAAACGATGAAACTGCAAAA

FIGURE 20

MDLAANEISIDYDKLSETVDLVRQTGHQCGMSEKAIEKFIRQLLEKNEPQRPPQYPLLIVVY
KVLATLGLILLTAYFVIQFSPPLAPEPVLGSAHTWRSLIHHIRLMSLPIAKKYMSENKGVPL
HGGDEDRPFPDFDPWWTNDCEQNESEFIPANCTGCAQKHLKVMLLEDAPRKFERLHPLVIKT
GKPLLEEEIQHFLCQYPEATEGFSEGGFFAKWWRCFPERWFPPYPWRRPLNRSQMLRELFPV
FTHLPFPKDALNKCFLHPEPVVGSKMHKMPDLFIIGSGEAMLQLIPPFQCRRHCSVAMP
IEPGDIGYVDTHWKVYVIARGVQPLVICDGTAFSEL

FIGURE 21

CCACGGTGTCCGTTCTTCGCCCCGGCGGCAGCTGTCCCCGAGGCGGGAGGAGCCCCGAGGGGCG
CGAGCCCCGCATGAATCATTGTAGTCAATCATTTTCCAGTTCTCAGCCGTTTCAGTTGTGATC
AAGGGACACGTGGTTTCCGAACGCCAGCTCAGAATAGGAAAATAACTTGGGATTTTATATT
GGAAGACATGGATCTTGCTGCCAACGAGATCAGCATTTATGACAACTTTTCAGAGACTGTTG
ATTTGGTGAGACAGACCGGCCATCAGTGTGGCATGTGAGAGAAGGCAATTGAAAAATTATC
AGACAGCTGCTGGAAAAGAATGAACCTCAGAGACCCCCCGCAGTATCCTCTCCTTATAGT
TGTGTATAAGGTTCTCGCAACCTTGGGATTAATCTTGCTCACTGCCTACTTTGTGATCAAC
CTTTCAGCCCATTAGCACCTGAGCCAGTGCTTTGTGGAGCTCAC

FIGURE 22

CCCACGCGTCCGCCACGCGTCCGGCTGAACACCTCTTCTTTGGAGTCAGCCACTGATGAGG
 CAGGGTCCCCACTTGCAGCTGCAGAGCTGTCAGCAGCTGCAGAGCGCTGCTCCTGGCTGGTG
 CCACTGGTGGCAGCGCTAGACCGTGCTATGAGCCGTGGGGCTGCAGTGGGGACTGCC
 CTCCTCTGCCACCCCAATGGCAGGCCACCTTCTTTGAAGACTTCAGAGGCTTTTGTGCCA
 CACCCGAATGGCGCCACTTTCATCGACAAACAGGTACAGCCAACTCCAGTCCAGTTCGAAATG
 GACACGTATGCTAAGAGCCAGCAGCTTATGTGAGGTTTCTGGAATGCCTGCTATGACATGCT
 TATAGCTAGTCGGCAGCGGCCCACTGGGAGCGCGCCAGAGTCTGTCGGCCCTTCCAGGAGC
 TGGTGTCTGGAACTGCGCAGAGGCGGGCGCGCTGGAGGGGCTACGCTACACGGCAGTGCTG
 AAGCAGGCACACGACGCACTCCATGGCCCTGCTGCACTGGGGGGCGCTGTGGCGCCAGCT
 CGCCACCCCATGTGGGGCTGGCGCTGAGGGACACTCCCATCCCCCGCTGGAACACTGTCCA
 GCGCCGAGACATATTACCGATCGCTGTAAGCTGGTGCCCAACCATCACTTCGACCCTCAC
 CTGGAAGCCAGCGCTCTCCGAGACAACTCTGGGTGAGGTTCCCTGACACCCACCGAGTGGCAGG
 CTCACCTGCCCTCTGGCAGTGACCAAGAGGCCAAAGTGAGCACCACCCGAGTGTGCTGCAGG
 AGGACACAGCTCGGCAGGACGAGCTGGCTGAGCTGGAGACCCCGATGGAGGCAGCAGAACTG
 GATGAGCAGCGTGAGAAGCTGGTGCTGTGCGCCGAGTGCCAGCTGGTGACGGTAGTGGCCGT
 GGTCCGAGGGCTGCTGGAGGTACCCACACAGAATGTATACTTCTACGATGGCAGCACTGAGC
 GGTGGAACCCGAGGAGGCGCTCGGCTATGATTTCCGGCGCCCACTGGCCAGCTGCGTGAG
 CTCACCTGCGCGCTTTCACCTGCGCCGTTCAGCACTTGAGCTTCTTATCTCATGACAGGC
 CAACTACTTCTCAACTTCCAGCTCAAGGTGGGCAGCACCAGCTCTCATCTTCTATGCCAGCA
 CTCGAGACCCAGCCTGGCCCACTCCACCCCATACCCAGGTACGGAACCCAGGTGTACTG
 TGGCTCTGCGCCCTACGCGCCCTCTCAAGGCTACCTAAGCAGCGCTCCCCCAGGAGAT
 GCTGCGTGCCTCAGGCCCTTACCAGAAATGGGTACAGCGTGAGATATCCAACCTCTCAGTACT
 TGAATGCTCTCAACACCATTTGCGGGGCGGACCTACAATGACCTGTCTCAGTACCTGTGTTG
 CCCTGGGTCTGCGAGGACTACTGTGTCCCAACCTGGACCTCAGCAACCCAGCGCTGTCCG
 GGACCTCTCTAAGCCCTCGGTGTGGTGAACCCCAAGCATGCCCAGCTCGTGAGGGAGAAAT
 ATGAAAGCTTTGAGGACCCAGCAGGGACATTGACAAGTTCCACTATGGCACCACACTCTCC
 AATGCACAGCGCTGATGCACCTACTCTCATCGCGCTGGAGCCCTTCACTCCCTGCAGCTCCA
 ACTGCAAGAGTGGCCGCTTTGACTGCTCCGACCGGCACTTCCACTCGGTGGCGGAGCTTGGC
 AGGCACAGCTGGAGAGCCCTGCCGATGTGAAGGAGCTCATCCCGAATTTCTTACTTTCTCT
 GACTTCTCTGGAGAACCCAGACCGGTTTTGACCTGGGCTGTCTCCAGCTGACCAACGAGAAGGT
 AGGCGATGTGGTGCTGACCCCGTGGGCCAGCTCTCCTGAGGACTTCATCCAGCAGCACCCGC
 AGGCTCTGGAGTCCGAGTATGTGTCTGCACACCTACACGAGTGGATCGACCTCATCTTTGGC
 TACAAGCAGCGGGGGCCAGCGCCGAGGAGGCCCTCAATGTCTTCTATTACTGCACCTATGA
 GGGGGCTGTAGACCTTGGACCATGTGACAGATGAGCGGGAACGGAAGGCTCTGGAGGGCATTA
 TCAGCAACTTTTGGGAGACTCCCTGTCACTGTGTAAGGAGCCACATCCAACCTCGGCTCTCA
 GCTGGAGGAGCAGCCCATCGCCTTGACGCTGGACACTAATCACTACCTAGCATCTTCCAGCA
 CCTGGAGCAACTCAAGGCATTTCTCGCAGAGGTGACTGTGAGTGGAGTGGGCTGCTGGGCA
 CCCACAGCTGGTTGGCTTATGACCCGCAACATAAGCAACTACTTCAGCTTCAGCAAGAGCCCC
 ACCATGGGCAAGCCACAAGACGACGAGCTGCTGAGTGGCCGCTGGGTGCCAGGAGCTGGTGT
 GAGTGGAGCAAGCACTGGCAGTGGCCCCGAGTGGAAAGCTGCTATTACGCGGTGGCCACTGGG
 ATGGACGCTGCGGGTGACTGCTACTACCCCGTGGCAAGCTGTTGAGCCAGCTCAGCTGCCAC
 CTTGATGTAGTAACCTGCCTTGCACTGGACACTGTGGCATCTACCTCATCTCAGGCTCCCG
 GGACACCACTGTGCTGGTGGCGGCTCCTGCATCAGGGTGGCTGTGTCACTAGGCTGGCAGC
 CAAAGCCTGTGCAGGTCTGTATGGGCAATGGGGCTGCAGTGTGAGCTGTGTGGCCATCAGCAT
 GAACCTGACATGCTGTGTCTGGATCTGAGGATGGAACCTGTGATACACACTGTACGCGG
 CGGACAGTTTGTAGCGGCACCTACGGCTCTGGGTGCCACATTCCTCGGACCTATTTCCGCC
 TGGCATTTGGGGTCCGAAGGCCAGATTGTGGTACAGAGCTCAGCGTGGGCAACGCTCTGGGGC
 CAGGTCACTACTCTTGCACCTGTATTCAGTCAATGGGAAGTTGCGGGCTTCACTGCGCCCT
 GGCAGAGACCTTACAGCCCTGACGGTGACAGAGGACTTGTGTTGCTGGGCAACCGCCAGT
 GCGCCCTGCACATCTCCAACTAAACACACTGCTCCCGGCCGCGCTCTTGTGCCCATGGAAG
 GTGGCCATCCGAGGCTGGCGCTGACCAAGGAGCGCAGCCAGCTGCTGGTGGGCTGGAGGA
 TGGCAGGCTCATCTGCTGGTGGTGCAGGGGCGAGCCCTCTGAGGTCGCGAGCAGCCAGTTCGCG
 GGAAGCTGTGGCGGTCTTCGCGGCCATCTCCAGGTTGCTCTGGGAGCAGCAAGTAACAAC
 CCTACTGAGGCGCGCTGAACCTGGCCAGTCCGGCTGCTCGGGCCCCCGCCCGCGAGCGCTG
 CGCCGGGAGGCCCGCCAGAAAGTTCGCGGGGAACACCCCGGGGTGGGCAAGCCAGGCGGTGA
 GCGGGGCCACACCTCGCCAGCTCAGGGATTGGCGGGCGATGTTACCCCTCAGGAGTGGGG
 GCGGGAAGTCCCGCTCCCGCTGAGGGGCGCCGCTGAGGGCCAGCACTGGCGCT

009990440.11401

FIGURE 23

MSQFEMDITYAKSHDLSMGFWNACYDMLMSSGQRRQWERAQSRRAFQELVLVEPAQRRARLEGL
RYTAVLKKQATQHSMALLHWGALWRQLASPCGAWALRDTPIPRWKLSSAETYSRMRLLKLVN
HHDFPHLEASALRDNLGEVPLTPTEEASLPLAVTKEAKVSTPELLQEDQLGEDELAELTF
MEAAELDEQREKLVLSAECQLVTVVAVVPGLEVVTTQNVYFYDGSTERTVETEEGIGYDFRRP
LAQLREVHLRRFNLRRSALELFFIDQANYFLNFPCKVGTTPVSSSPQTPRPQPGPIPHPTQV
RNQVYSWLLRLRPPSQGYLSRRSPQEMLRASGLTQKWVQREISNFEYLMQLNTIAGRTYNDL
SQYPVFPWVLQDYSPTLDLSNPAVFRDLSKPIGVNPKHAQLVREKYESFEDPAGTIDKFH
YGTHYSNAGVMHYLIRVEPFTSLHVQLQSGRFDCSRQFHSVAAAWQARLESPADVKEIIP
EFFYFPDFLENQNGFDLGCLQLTNEKVGDDVLPWPASSPEDFIQHRQALESEYVSAHLHEW
IDLIFGYKQRGPAEEALNVFYCYTEGAVDLDHVTDERERKALEGIIISNFGQTPCQLLKEP
HPTRLSAEEAAHRLARLDTNSPSIFQHLDELKAFFAEVTVSASGLLGTHSWLPYDRNISNYF
SFSKDPTMGSHKTQRLLSGPWPVPGSGVSGQALAVAPDGKLLFSGGHWGDSLRVLTALPRGKLL
SQLSCHLDVVTCALDTCGIYILISGSRDTCMVWRLHLHQGGLSVGLAPKPVQVLYGHGGAVS
CVAISTELDMAVSGSEDTGTVIIHTVRRGQFVAALRPLGATFPFGIIFHALHSEGQIVVQSSA
WERPGAQVITYSLHLYSVNGKLRLASLPLAEQPTALTVTEDFVLGLGTACALHILQNTLLPAA
PPLPMKVAIRSVAVTKERSHVLVGLGEDGKLIVVAGQPSSEVRSSQFARKLWRSSRRISQVSS
GETEYNPTEAR

N-glycosylation site.

amino acids 677-681

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 985-989

Tyrosine kinase phosphorylation site.

amino acids 56-65, 367-376, 543-551

N-myristoylation site.

amino acids 61-67, 436-442, 604-610, 610-616, 664-670, 691-697,
706-712, 711-717, 769-775, 785-791, 802-808, 820-826, 834-840,
873-879, 912-918, 954-960

CCGACGCGTGGGCGGACGCGTGGGGGCTGTGAGAAAGTGCCAATAAATACATCATGCAACCC
CACGGCCACCTTGTGAACTCCTCGTGCCAGGGCTGATGTGCGTCTTCCAGGGCTACTCAT
CCAAAGGCCTAATCCAACGTTCTGTCTTCAATCTGCAAACTCATGGGGCTCTGGGGCTCTTC
TGGACCCTTAACTGGGTACTGGCCCTGGGCCAATGCGTCTCTCGTGGAGCCTTTGGCTCCTT
CTACTGGGCTTCCACAAGCCCCAGGACATCCCTACCTTCCCCTTAATCTCTGCCTTCATCC
GCACACTCCGTTACCACACTGGGTCAATTGGCATTGGAGCCCTCATCTGACCCTTGTGCAG
ATAGCCCGGGTCACTTTGGAGTATATTGACCACAAGCTCAGAGGAGTGCAGAACCTGTAGC
CCGCTGCATCATGTGCTGTTTCAAGTGCTGCCTCTGGGTCTCTGGAAAAATTTATCAAGTTC
TAAACCGCAATGCATACATCATGATCGCCATCTACGGGAAGAATTTCTGTGTCTCAGCCAAA
AATGCGTTACATGCTACTCATGCGAAACATTGTCAAGGTGGTGTCTCTGGACAAAGTCACAGA
CCTGTGCTGTTCTTTGGGAAGCTGTGTTGGTGGTGGAGGCGTGGGGGTCTGTCTTCTTTT
TTTTCTCCGGTCCGCATCCCGGGGCTGGGTAAAGACTTTAAGAGCCCCACCTCAACTATTAC
TGGCTGCCCATCATGACCTCCATCTCTGGGGGCTATGTCATCGCCAGCGGCTTCTTCAGCGT
TTTCCGCATGTGTGTGGACACGCTCTTCTCTGCTTCTCTGGAAGACCTGGAGCGGAACAACG
GCTCCTTGACCGGCCCTACTACATGTCCAAGAGCCTTCTAAGATTCTGGGCAAGAAGAAC
GAGGCGCCCCCGGACAACAAGAAGAGGAAGAAGTGAAGCTCCGGCCCTGATCCAGGACTGC
ACCCACACCCACCGTCCAGGCATCCAACCTCACTTCGCCTTACAGGTCTCCATTTTGTGGT
AAAAAAGGTTTTAGGCCAGGCGCGTGGCTCACGCCTGTAATCCAACACTTTGAGAGGCTG
AGGCGGGCGGATCACCTGAGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGTGAACCTC
GTCTCTATTAAAAATACAAAAATTAGCCGAGAGTGGTGGCATGCACCTGTCACTCCCACTAC
TCGGGAGGCTGAGGCAGGAGAAATCGTTGAACCCGGGAGGCGAGAGTTCAGTGAAGCCGAGA
TCCGCGCCACTGCATCCAACCTGGGTGACAGACTCTGTCTCCAAAACAAAACAACAACAA
AAGATTTTATTAAGATATTTTGTGTAACTC

RTGRTRTGCGCEKVPINTSCNPHTAHLVNSSCPGLMCMVFQGYSSKGLIQRSVFNQLIYGVGLGF
WTLNWWVLALGQCVLGAFASFYWAHKPQDIPTEPLISAFIRTLRYHTGSLAFGALITLVQ
IARVILEYIDHKLGRGVNPARCICMCCFKCLWCLEKFIKFLNRNAYIMIAIYGNKFCVSAK
NAFMLLMRNIVRVVLDKVTDLLFFGKLLVVGGVGLSFFFFSGRIPGLGKDFKSPHLNYY
WLPIMTSLILGAYVIASGFFSVFGMCVDTLFLCFLEDLERNNGSLDRPYMYSSKLLKILGKNK
EAPPDNKKRK

FIGURE 26

GAGTCTTGACCGCCGCCGGGCTCTTGGTACCTCAGCGCAGCGCCAGGCGTCCGGCCGCCGT
 GGCTATGGTTCGTGTCGGATTTCCGCAAAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCC
 TTCTCTTCGTGGCCTCGGACGTGGATGCTCTGTGTGCGTGCAAGATCCTTCAGGCTTGTTT
 CAGTGTGACCACTGCAATATACGCTGGTTCCAGTTTCTGGGTGGCAAGAAGTTGAACTGC
 ATTTCTTGAGCATAAAGAACAGTTTCATTATTTTATTCTCATAACTGTGGAGCTAATGTAG
 ACCTATTGGATATTCTTCAACCTGATGAAGACACTATATTCTTTGTGTGTGACTCCCATAGG
 CCAGTCAATGTCTCAATGTATACAACGATACCCAGATCAAATTACTCATTAAACAAGATGA
 TGACCTTGAAGTTCCCGCTATGAAGACATCTTCAGGGATGAAGAGGAGGATGAAGAGCATT
 CAGGAAATGACAGTGTATGGGTGAGCCCTCTGAGAAGCGCACACGGTTAGAAGAGGAGATA
 GTGGAGCAAACCATGCGGAGGAGGACGCGCGAGAGTGGGAGGCCCGGAGAAGAGACATCCT
 CTTTGACTACGAGCAGTATGAATATCATGGGACATCGTCAGCCATGGTGATGTTTGAGCTGG
 CTTGATGCTGTCCAAGGACCTGAATGACATGCTGTGGTGGGCCATCGTTGGACTAACAGAC
 CAGTGGGTGCAAGACAAGATCACTCAAATGAAATACGTGACTGATGTTGGTGTCTGTCAGCG
 CCACGTTTCCCGCCACAACACCGGAACGAGGATGAGGAGAACACACTCTCCGTGGACTGCA
 CACGGATCTCCTTTGAGTATGACCTCCGCTGGTGTCTTACCAGCACTGGTCCCTCCATGAC
 AGCCTGTGCAACACCAGCTATACCGCAGCCAGGTTCAAGCTGTGGTCTGTGCAATGGACAGAA
 CGCGCTCCAGGAGTTCCCTTGACAGCATGGGTCTTCCCTGAAGCAGGTGAAGCAGAAGTTCC
 AGGCCATGGACATCTCCTTGAAGGAGAATTTGCGGGAAATGATTGAAGAGTCTGCAAAATAAA
 TTTGGGATGAAGGACATGCGCGTGCAGACTTTCAGCATTCATTTTGGGTTCAAGCACAAGTT
 TCTGGCCAGCGACGTGGTCTTTGCCACCATGTCTTTGATGGAGAGCCCGAGAAGGATGGCT
 CAGGGACAGATCACTTATCCAGGCTCTGGACAGCCTCTCCAGGAGTAACCTGGACAAGCTG
 TACCATGGCTGGAAGTCCGAAGAAGCAGCTGCGAGCCACCCAGCAGACCATTGCCAGCTGC
 CTTTGACCAACCTCGTCATCTCCAGGGCCCTTTCCTGTACTGCTCTCTCATGGAGGGCAC
 TCCAGATGTCATGCTGTTCTTAGGCCGGCATCCCTAAGCCTGCTCAGCAAAACCTGCTCA
 AGTCCCTTTGTGTGTTGCAAAAGAACCAGGCGCTGCAAACTGCTGCCCTGGTGATGGCTGCC
 CCCCTGAGCATGGAGCATGGCACAGTGACCGTGGTGGGCATCCCCCAGAGACCGACAGCTC
 GGACAGGAAGAACTTTTTGGGAGGGCGTTTGAAGGCAGCGGAAAGCACCAGCTCCCGGA
 TGCTGCACAACCATTTTGACCTCTCAGTAATTGAGCTGAAAGCTGAGGATCGGAGCAAGTTT
 CTGGACGCATTTATTTCCCTCCTGTCTTAGGAATTTGATTCTTCCAGAATGACCTTCTTATT
 TATGTAAGTGGCTTTCAATTAGATTGAAGTTATGGACATGATTGTAGATGTAGAAGCCATT
 TTTTATTAATAAAATGCTTATTTTAGGAAA

FIGURE 27

MFVSDFRKEFYEVVQSQRVLLFVASDVDALCACKILQALFQCDHVQYTLVPVSGWQELETAF
LEHKEQFHYFILINCGANVDLLDILQPEDTIFVCDSHRPVNVVNVYNDTQIKLLIKQDDD
LEVPAYEDIFRDEEEDEEHSGNDSGSEPSEKRTLREEEIVEQTMRRRQRREWEARRRDILF
DYEQYEHGTSSAMVMFELAWMSKDLNDMLWVAIVGLTDQWVQDKITQMKYVTDVGVLQRH
VSRHNHRNEDEENTLSVDCTRISFEYDLRLVLYQHWSLHDSL CNTSYTAARFKLSVHGQKR
LQEF LADMGLPLKQVKQKFQAMDISLKENLREMI EESANKFGMKDMRVQTF SIHFGFKHKFL
ASDVVFATMSLMESPEKDGSGTDHFTQALDSLRSNLDKLYHGLELAKQLRATQQTIASCL
CTNLVISQGPFLYCSLMEGTPDVMLFSRPASLSLLSKHLLKS FVCSTKNRRCKLLPLVMAAP
LSMEHGTVTVVGIPPETDSSDRKNFFGRAFEKAAESTSSRMLHNHFDLSVIELKAEDRSKFL
DALISLLS

27/330 - 27/330

FIGURE 28

GTACCTCAGCGCGAGCGCCAGGCGTCCGGCCGCCGTGGCTATGNTCGTGTCCGATTTCCGCA
AAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCCTTCTCTTCGTGGCCTCGGANGTGGAT
GCTCTGTGTGCGTGCAAGATCCTTCAGGCCCTTGTTCCAGTGTGACCANGTGCAATATANGCT
GGTTCAGTTTCTGGGTGGCAAGAACTTGAACTGCATTTCTTGAGCATAAAGAACAGTTTC
ATTATTTTATTCTCATAAACTGTGGAGCTAATGTAGACCTATTGGATATTCTTCAACCTGAT
GAAGACACTATATTCTTTGTGTGTGACACCCATAGGCCAGTCAATGTTGTCAATGTATACAA
CGATACCC

CGGTTTCTGAGTGGC

CAGGAACCCCTCTCTTTGGGTCGTGGATTGGGAACCTCTTTCCGATACCAATTTTTCCTAGTGAAC
CACAAGAGGCGCATACCGAAAAACCGCTCAACCCCAAAGGAATAAGATACATGACCCGCAATTTG
GCTGACTGTTTGGCTATAGAAAAAAGAAAGACCGAAAGAGACAGTTTTTTGGAAAGCTAA
GCTTCTCCCTTTATCGAGTCAGAAAGACCCCCCTCTTTCAGACTTTTACAGCTTTTAAACATTT
GAGTAAAGTAGCTGTCGGTACACCA**ATG**TGTCACAGCCGCCCTGGGTCGGCTTGGGACGGCTC
CTGCTCTTTTCTCTGTATGTGTGATAGTCGTATGTGGAGCTACCTTTGACAGAGCTGTGGC
CAGCGGCTGTCCAAACGCTGCTGTGACTCTGAGGCCATCTGTGATCTTCCGCTATGTCCTCAG
CCTCTTCTCTCCGGCGCCCGCCACCGCCCTTGGCTGATAGCTCAAGCCGTAACATACACCATC
CTGAAGGTTGACAAAGGGGACCCAGGCCCAATGGCCCTGACAAAGGGGATGACAAAGGGGAGATGGGACGCCCC
TCCCAAGAGGGGAGGCTTGGCCCTCAGGCCAGCAAGGGTGACAAAGGGGAGATGGGACGCCCC
CGCCCGCTGTGACAGAGCGCTTCTTCGCCCTCTCTGGCCGCTTGTGAACCTTGTGGGTGCTTTGA
CATGGCGACCGGGCGAGTTTGCTGCTCCCTCTGGCTGCTTACTCTACGCTCTCAATGTGTC
ACAGCTGGAAATTACAAGAGCGCTAGCTGCATATTCATCAACAGAAAGAGGCTGTATC
CTGTACGCCAGCCGACGAGGACGATACCTGTCAGAGCCAGAGTGTGATGCTGGACCTGGC
CTACGGGACCGCGTCTGGGTGGCGCTCTTCAACGCCAGCCGAGAAGGCCATCTACAGCA
ACGACTTGCACACTACATACCTTCTCAGCGGCCACTCATCAAGGCCGAGGACAGCT**GAG**GG
CCTCTGGGCCACCCCTCCCGGCTGGAGAGCTCAGTGTGGTCCGCTCCCTCGAGGGCTCAG
TTTGACTGCTGTGAAGCAGGAGGAGGCGAGGGCTCCCGCGGGAACCTGGCATCTGGGGAAC
CCCTGCTTCTATCTTGCTGGCTGCCATATCTCCAGCCTATTCTCTGCTCTCTCTTCTCTCT
TGGACCTATTTTAAGAAAGTTGCTATATCTCAAAATATTCTAGAATCTTCCAGCCCTCTGAGCC
AGCATCTTCTCAAACCTTGGAAATCTGCAATCTCCGCAATCACCGGGGTTCTGTGTAATGAGATTTCT
GACTCAGCAGGCTCTGATGGGTCCAGGAATCTGTFTTCTATGTTCTCTGGGTGATGCTG
ATGGGGTCAGTCTATGACCAACACTGAGCAACCAAGGTTCTAGGACTTTCTCAATATTTAG
TACTTTTCTGCAACTTCTGACCACTCTCCCAACTCTAGAAATTTCTCAAAATTTTCTTTCT
TGAGACAGAGTCTTGCTGCTCTTGGCCAGGCTAGAGTGCAGTGGTGCAATCTGATTTCACTGC
AACCTCTGCCCTCTGCTGCTCAAGCATTTCTTGCTCTCAGCCTCCATGTGGGCTGGGATATC
AGGCGCCTGCTACCATGCTGAGCTGCTAAATTTTGATTTTAGTAGAGTGGGTTTACCATA
TTGGCCAGGCTGTGTTTGAACTCTGACTTTCAGGTAGCCCAACCCGCTCGGCCCTCTCAAAAT
CGCTGGAGTCTGCTGTGAGCCACCGTGCCTGCCAATTTCAACATTTCTAAATTTCTCTCAT
CCTCCAGTCTGCTCCCGCTGCTATGTTCTTCTTACCCTTCCCTCTTCTCTCTGCTCAGGCC
TGCACTGCTGACGCGACCGTCTCAATTTATTCATTATAAACACTGAGCATCTGTTGCT
GGGTCCCGGAGAGGTTGAGGGGTGACAGCAAGGCCCTGCCCTGCCCTCAGTGAAGTGCCCA
GTTCCAGCCAGGCCGGGAGAGATGTGTACATAGTGTTTAAAGCAGACCCAGAGCTCATGGGG
GTTCTGTGTTCTGGGTGTTCAAGTGCTGTGCTCTCTTATACCACTGCTCCCCAAGGCTGG
TGGGACGGGTCCCGGTGCGAGGGCGAGTTATCTCTTCCGTTTCTCATCACTCCGACGCCAG
TGCTCTCTGTTACAGCAACCCCAAGGGGGCTTGGCCAGTCAAGGGTCTGTGAGGAGAGG
ACCCAGAGTGTGGGGGCTTTGGGGGGTGAGTGGCCCCGAAGAAATGGAACCAACCCCA
TAGCTCTCCCACTAGTACATGGCATCTGCGAGGAAGCACTGCCCTCTCTCACTGGGATCTC
TCTTCTGCCCTCTCCAGGGCTCTGCCAGGCCCTGTGCTAGTCCCTTCCCAAGGTCTATCT
GAACTTCCGTTTCCCCAGGGCTCCAGGCTGCCCTCAGACACTGATGTCTGTCCGCCAGGTGCT
CTCTGCCCTCTATGCCCTCTACACGGCCGAGTGCCCGACTCTCAGGGTTTATCAAGGTG
CTAAGGCTCCGGGTGGGCGACTCTCTGPTCTCAGAGCCCTCTCCCGGCTGGTGTGCTCTTATC
AAACACTCGCAGGAGAAGGGCCACGGAAGCCCGAGGCTTTAGAGCCCTCAGCAGGTTCTGGGG
AGCTAGACCAAGAGGAGGACCTCAGGCTCTCCGTTTCTTCTTCCAGGGTGGGGTGGCTTGGT
GTTCCCTAGCTCTTCCAACCAAGGCTGGCCTGCGCTTCTCCCAAGAGGAGGCGGCTCCGC
CCATTTGTTGCTCATGCACTCTGGGGCTGAGGTGCCCGGGGGGTGATCTCTGGTGTCTAC
AGCCGAGGGAGCGGTGGACTTCATGGCCAGATGACGGAACCAAGGTTGATCCAAAGTGGCAGGA
AGACCTTGCTGTTAAACCACTCTGCCGTGATCTCGGCTGCTGCTACCCCGCCAGCCCTGCC
GTCCAGCATGATTAAGAATGCTGCTCTCTCTTGAAAAAATAAAAAA

FIGURE 30

MVTAALGPVWAALLFLLMCEIRMVELTFDRAVASGCQRCCDSEDPLDPAHVSSASSSGRPH
ALPEIRPYINITILKGDKGDPGMPGLPGYMGREGPQGEPPGPQGSKGDKGEMGSPGAPCQKRF
FAFSVGRKTALHSGEDFQTLLFERVFNLDGCFDMATGQFAAPLRGIYFFSLNVHSWNYKET
YVHIMHNQKEAVILYAQPSESRIMQSQSVMLDLAYGDRVWVRLFKRQRENAIYSNDFDTYIT
FSGHLIKAEDD

Important features:**Signal peptide:**

amino acids 1-20

N-glycosylation site.

amino acids 72-75

Clq domain proteins.

amino acids 144-178, 78-111 and 84-117

CC-BY-NC-ND 4.0 International license

FIGURE 31

ACTCGAACGCGAGTTGCTTCGGGACCCAGGACCCCTCGGGCCGACCCGCCAGGAAGACTG
AGGCCCGCGGCTGCCCGCGCGGCTCCCTTGCGCCGCGCGGCTCCCGGGACAGAAAGATGTG
CTCCAGGGTCCCTCTGCTGCTGCTGCGGCTGCTCTCTGCTAGCGCTGGCCCTGGGTGAGG
GCTGCCCATCCGGCTGCCAGTGCAGCCAGCCACAGACAGCTCTTCCAGCTGCCCGCCAGGGG
ACCACGGTGCCCGGAGAGCTGCCACCCGACACGGTGGGGCTGTACGCTCTTTGAGAACGCAT
CACCATGCTGCAGCGAGGACGTTTTCGGCGCTGCGCGGCTGACGCTCTTGAGCTGTAC
AGAACCAGATGCCAGAGCTGCCACCGGGGTCTTCAGCGCACTGCCCAACCTCAGCAACCTG
GACCTCAGCGCCAAAGCTGTGATGAATCACCATTAGACATCTCCGTGGGCTGCGGCGCG
CGAGCGCCTCTAAGTGGGCAAGAACCGCATCCGCCACATCCAGCCTGGTGCTTGCACACG
TCGACCGCCTCTTGAGGACTAAGCTGACGAGCAACAGAGCTGGGGCACTGGCCCCGCTGCG
TGCCCCGCTGCTGCTGCTGAGACTCAGCCACCAAGACGCTCTGGCCCTGGAGCGCGGAT
CCTGGACATCGCCAACGTTGAGGCGCTGCGGCTGCTGCTGGGTGCGAGCAGCTGCAGC
AGGGGCTCTTACGGCGTTGCGCAACCTCCAGCACTGGATGTGTCCGACCAACAGCTGGAG
CGAGTGCCACCTGTATCCGAGGCTCCGGGGCTGACGCGCTGGGCTGGCCGGCAACAC
CCGCATTTGCCAGCTGCGGCCCGGAGGACCTGGCGCGCTGGCTGCCCTCGAGGAGCTGATG
TGAGCAACCTAAGCTCGAGGCGCTGCTGCGGCTGCTGCGGCTCTTCCCGCTGCGG
CTGCTGGCAGCTGCCCGCAACCCCTTCAACTGCGTGTGCCCTCGAGCTGGTTTGGCCCCG
GGTGCGCGAGAGCGCACTCACAATGGCCAGCTTGAGGAGACGCGCTGCCATCTCCGCCCA
AGAACGCTGGCCGCTGCTCTTGAGGCTGTACTAGCCGACTTTGGCTGCCAGGCCACAC
ACCACAGCCAGAGCTGCCCAACCCAGGCGCGGTGTGCGGAGGCCCAAGCCTGTGTTCTAG
CTTGGCTCCTACCTGGCTTAGCCCCAGGCGCGGCACTGAGGCCCGCCAGCTCCCTCTCA
CTGCCCAACCGACTGTAGGCGCTGTCCCCAGAGCCAGGACTGCCACCGCTCCACCTGCTC
AATGGGGGCTACCTCAACCTGGGCAAGCCAGCCACCTGGCTGCTTTGGCCGCAAGGGTT
CAGGGGCTGTACTGTAGAGCCAGATGCGGAGGGGACAGCCGCAACCTACACGATCA
CGCCGAGGCCACCAAGTCCCTGACCTGGGCACTGAGCGGCTGAGGCCCACTCCCTGCGC
GTGGGGCTGACAGCGCTACCTCGAGGGGAGTCCGTGACGCTCAGGAGCTCCGCTTCACTA
TCGCAACCTATCGGCGCTGATAAGCGCTGGTGACGCTGCGACTGCTGCCCTGCTGCTG
AGTACAGGCTACCAAGCTGCGGCCAGCAACGCCACTTACTCGTCTGTGTCATGCTTTGGG
CCCCGCGCGTGCAGGAGGCGAGGAGCTGCGGGAGGGCCATACACCCAGCGCTCCA
CTCCAACCAAGCCCAAGTACCCAGGCCGCGAGGCAACCTGCCCTACTATTGCGCCCG
CCCTGGCGCGGTTGCTCTGCGCGCTGCGTGGTGGGGGAGCCCTACTGTGCGGCG
GGGCGGCGCATGCCAGCGGCTCAGGACAAAGGGCAGGTGGGGCAGGGGCTGGGCGCT
GGAATCGAGGGAGTGAAGTCCCTTTGAGGACAGGCCGGAAGGCAACAGAGGCGGTGGAG
AGGCCCTGCCAGCGGCTGAGTGTGAGGTGCCACTATGGCTTCCAGGCGCTGGCCTC
CAGTACCCCTCCACGCAAGGCCCTACATCTAAGCCAGAGAGACAGGCGAGCTGGGCGG
GGCTCTCAGCGAGTGAAGATGGCCAGCCCTCTGCTGCGCACACAGCTAAGTTCTCAGTCC
CAACCTCGGGGATGTGTGACAGAGGCTGTGTGACCAAGCTGGGCGCTTTCCTCTGGA
CCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCAGCTGACGAGCCTTAAGTCCCCAGAAC
CGAGTGCCATGAGGACAGTGTCCGCGCTGCCCTCCGCAACGTGACGCTCTTGGCAGCGG
GGCCTGCCATGTGCTGTGATACGCAATGCTTGGGCTCTGTGGCTCTCCACTCAGGCGGA
CCCTGGGGGCGAGTGAAGGAAGTCCCGGAAGAAGCAGAGGAGAGCGGGTAGGCGGTGTG
TGACTTAGTCTTGCCCGCAGGAGCGAAGGAACAAAGAACTGGAAGGAAGTGTCTTAT
GGAACATGTTTTGCTTTTTTAAATATATATATTTATAAGAGATCCTTCCGCTTTATTCTG
GGAAGATGTTTTTCAACTCAGAGCAAGGACTTTGGTTTTTGTGTAAGACAACGATGATATG
RAGGCTTTTTGTGAAGAAAAATTAAGATGAAGTGTGA

MCSRVPFLLLPLLLLLLALGPGVQGCPSGCGCSQPQTVFCTARQGTTVPRDVPDVTGLYVFEN
GITMLDAGSFAGLPGLQLLLDSQNQIASLPSGVFQPLANLSNLDLTANRLHEITNETFRGLR
RLRLRYLKGKNRIRHIQPGAFDTLDRLELEKLQDNELRALPPLRLPRLLLLDLSHNSLLALEP
GILDTANVEALRLAGLGLQQLDEGLFSRLRNHLHDLDVSDNQLERVPPVIRGLRGLTRLRLAG
NTRIAQLRPEDLAGLAAQLQELDVSNLSLQALPGDLSGLFPRRLRLAAARNPFNCVCLPSWFG
PWVRESHVTLASPEETRCHFPKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALS
SSLAPTWLSPTAPATEAPSPSTAPPTVGPVPQPQDCPPSTCLNGGTCHLGRTHHLACLCFE
GFTGLYCESQMGQTRPSPTPTVTPRPRSLTLGIEPVSTSLRVLGRLYLQGSVVGLRSLRL
TYRNLSPGDKRLVTLRLPASLAEYTVTLRPNATYSVCVMLRPGRVPGEAGEACBHAETPPA
VHNSHAPVTQAREGNPLLIAPALAVVTLAALAVGAAYCVRGRGRAMAAAAQDKGQVGPAG
PLELBGVKVPLEPGPKATEGGEALPSGSECEVPLMGFPGLQSPHLAKPYI

FIGURE 33

GAATCATCCACGACCTGCAGCTCTGCTGAGAGAGTGCAAGCCGTGGGGGTTTTGAGCTCAT
 TCTTCATCATTATATAGGAAATAAGTGGTAAAACTCTTGGAAATACATGAGACTCATCAG
 AAACATTTACATATTTTGTAGATTGTGTATGACAGCAGAGGTGATGCTCCAGAGCTGCCAG
 AAGAAGGGAACATGATGACCACTGCTCCAACATGTCTCTAAGAAAGGTTCCCGCAGACTTG
 ACCCGACCAACGACACTGGATTTATCTATAACCTCTTTTCACTCCAGAGTTCAGA
 TTTTCATCTGCTGCTCAACACTGAGAGTTTGTATTCTATGCCATAAACAATTCACAGCTGG
 ATCTCAAACTCTTGAATTCACAAAGGAGTTAAGATATTTAGATTGTCTAATAACAGACTG
 AAGAGTGTAACTTTGGTATTTACTGGCAGTCTCAGGTATTTAGATCTTTCTTTTAATGACTT
 TGACACCATGCTTATCTGTGAGGAAGCTGGCAACATGTACACCTGGAAATCTCAGGTTTGA
 GTGGGGCAAAAATACAAAAATCAGATTTCCGAAAAATTGCATCTGCATCTAAATCTGTC
 TTCTTAGGATTGAGAACTCTTCCCTCATTATGAGAAGGTAGCCCTGCCATCTTAAACACAC
 AAAACTGACATTTGTTTTACCAATGGACACAAATTTCTGGGTCTTTTGCCTGATGGAATCA
 AGACTTCAAAAATTTAGAAATGACAAAATATAGATGGCAAAAGCCAATTTGTAAGTTATGAA
 ATGCAACGAAATCTTAGTTTGAAGAAATGCTAAGACATCGGTCTTATTGCTTAATAAAGTTGA
 TTTACTCTGGGACGACCTTTTCCCTTATCTTACAATTTGTTTGGCATAACAGTGGAACTAC
 TTCAGATCCGAAATGTGACTTTTGGTGGTAAGGCTTATCTTGACCACAAATTCATTTGACTAC
 TCAATTAAGTGAATGAGAACTATAAAATGGAGCATGTACATTTAGAGTGTTTTACATTCA
 ACAGGATAAAATCTATTGCTTTTGACCAAAATGGACATGAGAAACCTGACATATCAAAATG
 CACAAATGCGCACATGCTTTTCCGAAATATCTCAGAAATTTCAAAATTTTAAATTTGGC
 AATAATATCTTAAACAGACGAGTTGTTTAAAGAACTTCCAACCTGCCCTCACTTGAACACTCT
 CATTTTGAATGGCAATAAATCGGAGACACTTTCTTAGAAGTGTCTTGTACACACACAC
 CTTTGAACACTTGGATCTGAGTCAAAATCTATTACAACATAAAATGATGAAATTTGCTCA
 TGCCGAGAACTGTGGTCAATATGAATCTGTATCAATAAATTTGCTGATTCTGCTCTCAG
 GTGGCTGCCCAAAAGTATCAAACTCTGACCTAAATAAATCAACAAATCCAACCTGTACCTA
 AAGAGACTATCTATCTGATGGCTTTACGAGAACTAAATATTGCAATTTAATTTCTAACTGAT
 CTCCCTGGATGCTGAGTCAATTTAGTAGACTTTCAGTTCTGAACATTTGAAATGAACTTCACTT
 CAGCCCATCTCTGATTTTGGTTTCCAGAGCTGCCAGGAAGTTAAACCTCTAAATCGGGGAAGAA
 ATCCATTCGGGTGTACCTGTGAATTAATAAATTTTCACTCAGCTTGAACATATTCAGAGGTG
 ATGATGGTGGATGCTAGATTCAATACACCTGTGAATACCTTTAAACCTAAGGGGAACCTAG
 GTTAAAGAGCTTCACTCCACGAATTTATCTGCAACACAGCTCTGTTGATTTGCCACCTTG
 TGCTTATTAAGTGTAGTTCTGGGGTTGGCTGTGGCCTTCTGCTGTCTCCACTTTGATCTGCC
 TGGTATCTCAGGATGCTAGGTCAATGCACACAAACATGGCACAGGGTTAGGAAAAACAACCCA
 AGAACAACTCAAGAGAAATGTCGATTTCCACGATTTATTTTATACAGTGAACATGATTTCT
 GTTGGGTGAAGAATGAATGTATCCCAATCTAGAGAAGGAAGATGGTTCTATCTGATTTGTC
 CTTTATGAAAGCTACTTTGACCTTGGCAAAAGCATTAGTGAAATATTGTAAGCTTCATTGA
 GAAAAGCTATAAGTCCATCTTTGTTTGTCTCCCACTTTGTCCAGAATGAGTGGTGCCATT
 ATGAATCTACTTTGGCCACCAATCTCTTCCATGAAAATTTGATCATATAATCTTTATC
 TTTACTGGAACCCATCCATTTCTATTGCAATCCCAACAGGATCATATAACTGAAAGCTCTCT
 GGAAAAAAGCATCTTTGGAATGGCCAGGATAGGCGTAAATCTGGGCTTTTCTGGGGCA
 ACCCTCGAGCTGCTTAAATGTTAATGTATTAGCCACAGAGAAATGTATGAACTCGAGACA
 TTCACAGAGTTAAATGAAGAGTCTCGAGGTTCTACAATCTCTGATGAGAACAGATTTGCT
 ATAAATCCCAAGCTCTTTGGGAAATTTGGGGACACATACACTGTTGGGATGTACATTTGATA
 CAACCTTTATGATGGCAATTTGACAATATTATTAATAAATAAATGTTATTCCCTTATA
 TCAGTTTCTAGAAGGATTTCTAAGAAATGTATCCTATAGAAAACACCTTCACAAGTTTATAAGG
 GCTTATGGAATAAGGTGTTCTATCCAGGATTTGTTTAAATCAATAAATAATGTGGCCAGGTGC
 AGTGGCTCACTCTGTGAATCCAGCACTGTGGGAGGCCAAGTGGGTGCCACCGAGGTCAA
 GAGATGAGACCATCTTGGCCAACTGGTGAACCCGTCTCTACTATAAATAACAAAATTA
 GCTGGGGCTGATGTTGCAAGCTGTAGTCCAGCTACTTTGGGAGGCTGAGGCAGGAGGATCG
 CTTGAAGCCGGGAGGTGGCAGTTGCACTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGT
 GACAGGCGGAGACTCCATCTCAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAATCAATCC
 TCATGGCCCAAAAAATAAGGTCTAATTCATAAATATATAGTACATTAATGTAAATATAATATTA
 CATGCCACTAAAAAGAAATAGGTAGCTGTATTTCTGGTATGAAAAAACATATTAATAT
 GTTATAAATATAGGTTGGTGCAAACTAATGTGGTTTTGTCATTGAAATGGCATTTGA
 ATAAAGGTGAAAGAAATCTATACCAGATGTAGTAACAGTGGTTGGGTCTGGGAGGTGGA
 TTACAGGAGCATTTGATTTCTATGTTGTATTTCTATAATGTTTGAATGTTTGAATGTA
 ATCTGTATTTCTTTTATAGTAGAAAAAATAAAGATAGTTTTTACAGCTT

09990440.11401

MRLIRNIYIFCSIVMTAEGDAPELPEERELMNCNSMLRKVPADLT PATTTLDLSYNLLFQ
 LQSSDFHVSVKLRVLILCHNR IQQLDLKTFEFNKELRYLDLSNNRLKSVTWYLLAGLRYLDL
 SFNDFDTPMPCIEEAGNMSHLEILGLSGAKIQKSDFOKIAHLHLNTVPLGFRTLPHYEEGSLP
 ILNTTKLHIVLPMDFTNFVLLRDLGDKTSKILEMTNIDGKSQFVSYEMQRNLSLENAKTSVLL
 LNKVDLLWDDLFLILQFVWHTSVEHFQIRNVTFGGKAYLDHNSFDYSNTVMRTIKLEHVHFR
 VFYIQDQKIYLLLTCKMDIENLFTISNAQMPHMLFPNYPTKFQYLN FANNILTDELFKRTIQLP
 HLKTLILNGNKLETL SLVSCFANNTPLEHLDLSONLLQHKNDENC SWPETVVMNLSYNKLS
 DSVFRCLPKSIQILD LNNNQIQTPKETIHLMALRELNIAFNFLTDLPGCSHFSRLSVLNI E
 MNFILSPSLDFVQSCQEVKTLNAGRNPFRCTCELKNFIQLEYSEVMVMGWSDSYTC EYPLN
 LRGTRLKDVHLHELSCNTALLIVTIVVIMLVGLAVAFCCFLHFDLPWYLRMLGQCTQTHRV
 RKTTEQELKRNVRFHAFISYSEHDSLWVKNELIPNLEKEDGSILICIESYFDPGKSIENI
 VSFIEKYSKIFVLSPNFVQNEWCHYEFYFAHNNLFHENS DHIIILEPFIYPFYCIPTRYHK
 LKALLEKKAYLEWPKDRRCGLFWANLRAAINVNVLATREMYELQTFTELNEESRGSTISLM
 RTDCL

GGGGGCTTTCTTGGGCTTGGCTGCTTGGAAACACTGCTCTCAAGGACCGGCTCGGAGGGGTCGCGGGAAAGG
CAGGAGAAAGAAAGGCGGGGCGGCGCCCTCTGCGCCGCGCCGCGCTCTGCGCGCCCTGTCTCGCCCGGCG
CGAGCGACCGCCAGCCCGCGCGCGGTTCACAGCGACGACGCGCGCGCTCCGCGCGCCAGCGCGCGGCT
CTGCTGCTGCTGCGCCCTTGCCCGCGGCACTTCTGCGCGCGACGCGCGCGCGCGCGCGCGCGCTGCA
CCCTGCTCCGGGCGGGGCGAGCGAGCTGTCGCGCGGGGACCGCTACCCAGCGCTGGGCTGTGTCGT
CTGGACGTGAGGCTGCGCGGGTGGAGCGCCAGGCGAGCGCTCGAGGACCGCTGATTATTGCGCGGAGGAT
CTGGAGCGACCGGACCTATACGCGCGCGGAGCCGAGCTCAGAGACTCTCTCTGCGCGCTGCTGCGGGG
CGCGGAGGAGTGGGAGCGGCGCGCGAGGAGCGCGCGCGCCAGGAGGCGCCAGGCGCAAAAGCTCCC
AAGAGGAGAACTCGGCTCGGAGCGCGCTCCACAGTGAATACAGCAGCAAAAAAGTTATGAGAACAAAGA
CTCTGAGAAGCTGCCAAGTAGTACAGTGTCTGCTGTGGCGGCGAAGATGTACAGAGAGATGTGCCAAT
TTGGTCTGGAAACTTAAAAATCAGACTTTCAGCTCCATGCTCCAGCTGAAGCGATGTGCGCTGGGGGA
CATCGAGGAGACTCACATCCAGCGGGCATGTATAAAATGATTATTATGAGCAATGACAGCCCACTGGTGT
AAATGACTCTCAGACTGTGATGAAGTGATGTGCGCTGACGAGTGTGAGTGAAGTCTGATGAATGAGT
ACCGCTCCCATGTGGGCGCGTACATCCGCAATAACCTCAGTCTGTTGATATGGAGACTCATGATGA
GATGAGATCTCTGGGCTGCCACTCGCAGTCTAATAATTATTATCCCGCGGAACGAGTACGCCACTG
GATGCCCTGGATTTTAAGCACCAAAATTAAGAAGTACGCCAGTGTGATGAAGTCTGCTGAGATCTCAGAT
CATATTCACAGAATTTACAACTTGAAAAAGCCACCGAGCGCTGAAGCTGTGATGAATGAGTGTGCC
ACCTGGGAGAGCATGAAGTCGGTAGGCCAGTTCACATCATCGCGGGGCGACGCGCAATGAGTGTCTGGC
CGGAGACTGCTGCTGTGCTGTGTCAGTGTCTGTGTTCAGGATGACTTGGCGGGAATCGGCGCATCTGTC
GTTGGAGAGAGCGGATTCAGTCTCCCTCCCTCACCCGAGTGTGCTACGAGAGCGCTACGAGGGGCT
CGGAGCTGGGAGCTGTTCCCTGGAGCTGAGCGACCATGAGTGAATTCACATCAACAACTGATGCTATT
ACAAGCTGCTCTGGGAGCGAGAGTACAGAGACTGTCCCGAAGAAATGCCAATCATTATTTGCAATTC
TGAGTGGTTTCTGTGCGAAAAATGCGAGCTGGTCTGCCGAGAGCGAGAGTATACGCTGGATGGAAAAATC
TTTTTGTCTGGGCGAACTCGAGGCGGGGCGAGCTGTGTCGAGGATTCCTACAGCTGTTGGTGGTCCCC
TGGAAGCGCAGGAAAGCAACCCCCAGCCCATGACCACTGCTTCGCTGGCTGAGCTCCTCTGCTCCAC
ACAGCGCTCATTCAGACAGCGCGCGAGGAGGGTGTGCCACGAGGAGTCTCAGAGAGGAGAGGAGCTGTCA
ITGGGGCTCTTGCGCACAGCTGCTGGAAGTCTGAGACGATTTCAGCTACTTCATCAAACTGCTTCGAAGT
TCCATCTAGTGGGCTGTATAAATCCACATGAGGAGAGCTGCCCGAGGATGGGAAATACCGGGAATC
TCTGATGCTTTCAGGAGCAGTGTTCATGTCGTATTAAGGCTTGTGAGAGATTACATGTGAAGAAAGATCC
CAAACTGCCATTATCTCGTAGAGGCATTAACTCATCATCCGACGCAAGTGGGGAATCTGGCGGCTCT
CTGAACGCTGGAGATGTGTTCAAGAAAGGCGCGAAGTTCATGCTACCCAGAAAGCTGTATGTTGGT
CTATGACATGGGGCCACAGTGTGTAATCTACACTTCAGAAAACCAATGCGCAGGATCGAGAGATGCG
AGAATTTTGGGAGACGCGCGTCAAGCTCGGACGAGGCGGCTGAAGCTCGGGGGCGGAAGACAGACAGGCT
GGGTCGACCTCTGCGCCCTTGAGACTCTGCGGACATGCAAAATTAACCAACTGTTAGTGTGCTCATG
TGGCTCATCTACCTGTTTCTTCTGTAATCAAGAAGTGCTGGAGAGAGGGTGCAATGTGAGGCGCTCC
CAAAAGGGAAGCTGGAGCTGAGGCTGTTTCTTCTTCTGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT
CAGAGAAAAGATGATGGGAGTGAGAGAACTCAGCAAGCAACTGCGGAATCAGAGAGAGGAGGAGGAGG
GAGGCTGTGCTTCAGAGCTCTGGCTCGATGAAAGGATCTGTCCTGCTTCTGCTGCTGCTGCTGCTGCTG
TCTCCAGTGCATTTTCAATTTCGACATGCAATTTGCACTTTCCCGAGCTGGGCTGCCCAATGTATCA
TTGAGATGCTCCGAGGCTGCTAAGAAATCCACCTCTCTGCGCTGGACATCGAAGCTGCAATAAA
ATTCTGTGTTTGTGAAATAGCTGTCATTGCCAAGTGCATCAGTGAAGCTCTTGAATCTGTTTACTCTCT
TTTTCACAAAGGAGTGTTTCAGAAAAGGAGAGGCGTGAATCATCAGAGTATTGTTGGGACCAAGCA
TGGAGCTTCTGCAAAATCTGGGTCATAAAACCCCAAAGTCCCTGCTGATTCAGTACGCTGAGGCTT
CCCCAGTAGGAGAGCGAGAGTGGCCAGCTTCTGAAGGCGCAAGAAATTTAGCTGGATCTCTCTTTAC
TGCTAGGACTGAAAGAGCGAGAGTGGGTTGGCTGAGGCCCTCTCTGCTGAGGATTTGCCCTGTGTG
GAATTGAGTGTGCTGGTGGGCTCATATGACCTGAGGATTTTGTATGTGGAAGATGCAATCTTCCA
GATTAGGCTAAATGTAAATGAACCTCTAGGATTCCTGTGAGCATGTTGTGGGAAAGATTGAATTA
CTTGCAGAAAAAGATGTCTCATTTTGTGTAATGTTGCTGCTCATGAGCTGGGAAAAAGAAAAAA
AATAAGCAAAATGTAAGACCTTAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA

FIGURE 36

MSRPGTATPALALVLLAVTLAGVGAQGALEDPDYYGQEIWSREPYARPEPELETFSPLP
AGPGEWERRPQEP RPPK RATKPKKAPKREKSAPEPPPGKHSNKKVMRTKSSEKAANDDHS
VRVAREDVRESCPLGLETLKITDFQLHASTVKRYGLGAHRGRLLNIQAGINENDFYDGAWCA
GRNDLQQWIEVDARRLRTFTGVITQGRNSLWLSDWVTSYKVMVSNDSTWVTVKNSGDMIF
EGNSEKEIPVLNELPVPVMVARYIRINPQSWFDNGSICMRMEILGCPLPDPNYYHRRNEMTT
TDDLDFKHHNYKEMRQLMKVVNEMCPNITRIYNIGKSHQGLKLYAVEISDHPGEHEVGEPEF
HYIAGAHGNEVLGRELLLLLVQFVCQEYLARNARIVHLVEETRIHVLPSLNPDGYEKAYEGG
SELGGWSLGRWTHDGDIDNNNFPDLNTLLWEADRQNVPRKVPNHYIAIPEWFLSENATVAA
ETRAVIAWMEKIPFVLGGNLQGGELVVAYPYDLVRSPWKTQEHTPTPDDHVFRWLAYSAST
HRLMTDARRRVCHTEDFQKEGTVNGASWHTVAGSLNDFSYLHTNCFELSIYVGCDKYPHES
QLPEEWENNRESLIVFMEQVHRGIKGLVRDSHGKGINAIISVEGINHDIRTANDGDYWRLL
NPGEYVVTAKAEGFTASTKNCMVGYDMGATRCDFTLSKTNMARIREIMEKFGKQPVSLPARR
LKLGRKRQRG

FIGURE 37

CTAAGAGGACAAGATGAGGCCCGGCTCTCATTTCCTAGCCCTTCTGTCTCTCTTGGCCAAGCTGCAGGGG
 ATTTGGGGGATGTGGGACCTCCAATTCCAGCCCCGGCTTCAGCTCTTCCAGGTGTTGACTCCAGCTCCAGC
 TTCAGCTCCAGCTCCAGCTCGGGCTCCAGCTCCAGCCGAGCTTAGGCAGCGGAGGTTCTGTGTCCCGATTGTT
 TTCAAATTTCCAGCGCTCCGTGGATGACCGTGGGACCTGCCAGTGTCTGTCTCCCTGCCAGACACCACTTTTC
 CCGTGGACAGATGGAACGCTTGGAAATTCACAGCTCATGTTCTTCTCAGAACTTTAGAAAAGAACTTTCTAAA
 GTGAGGGAATATGCTCAAATTAATAGTGTGTATGAAAAGAACTGTAAACCTTAACGTGTCGAATTGACATCAT
 GGAGAAGGATACATTTCTTACACTGAACTGGACTTCGAGCTGATCAAGGTAGAGTGAAGGAGATGGAAAAC
 TGCTCATACAGCTGAAGGAGAGTTTGGTGGAGCTCAGAAATGTTGACCAAGCTGGAGGTGGAGATAAGAAAT
 ATGACTCTCTTGGTAGAGAAGCTTGAGACACTAGACAAAACAATGTCCTTGCCATTGCGCGAGAATCGTGGC
 TCTGAAGACCAAGCTGAAAGAGTGTGAGGGCTCTAAAGATCAAAACACCCCTGTCGTCCACCTCCCTCCACTC
 CAGGGAGCTGTGGTCTATGGTGTGGTGAACATCAGCAAACCGCTCTGTGTTTCAGCTCAACTGGAGAGGGTTT
 TCTTATCTATATGGTGTGGGGTAGGGATTACTCTCCCGAGCATCCAAACAAAGGACTGTATGGGTGGCGCC
 ATTTGAATACAGATGGGAGACTGTTGGAGTATTATAGACTGTACAACACACTGGATGATTGCTATTGTATATAA
 ATGCTCGAGAGTTGCGGATCACCTATGGCCAAAGTAGTGGTACAGCAGTTTACAACACACACATGTACGTCAAC
 ATGTACAACACCGGGAATATTGCCAGAGTTAACTGACCACCAACACAGGATTGCTGTGACTCAAACTCTCCCTAA
 TGCTGCCTATAATAACCGCTTTTCATATGCTAATGTTGCTTGGCAAGATATTGACTTGGCTGTGGATGAGAATG
 GATTGTGGGTATTATTCACTGAAGCCAGCACTGGTAACATGGTGATTAGTAACTCAATGACACCACTT
 CAGGTGCTAABCACTTGGTATACCAAGCAGTATAAACCATCTGCTTCTAACGCGCTTCATGGTATGTGGGGTTCT
 GTATGCCACCCGTACTATGAACACCAAGAACAGAGAGATTTTTACTATTATGACACCAACAGGGAAGAGG
 GCAAACTAGACATTGTAATGCATAAGATGCAGGAAAAGTGCAGAGCAATTAACCTTTTGAACAGAAA
 CTTTATGTCTATAACGATGTTTACCTTCGAATTATGATCTTTCTGTCTTGAGAGAGCCCCAGTAAAGCTGTTTA
 GGAGTTAGGGTGAAGAGAAAATGTTTGTGAAAAATAGCTCTTCCACTTACTTAGATATCTGCAGGGGTGT
 CTAAAAGTGTGTTCAATTTGCAGCAATGTTTAGGTGCATAGTTTACCACACTAGAGATCTAGGACATTTGTCT
 TGATTTGGTGAGTCTCTTGGGAATCATCTGCCTCTTCAGGCGCATTTTGCAATAAAGCTGTCTCAGGTGGGA
 TTGTGAGAGTCTAGGGGCACTGTGGGCTAGTGAAGCCTACTGTGAGGAGGCTTCACTAGAAGCTTAAATTA
 GGAATTAAGGAACCTTAAACTCAGTATGCGCTCTAGGGATTCTTTGTACAGGAAATATTGCCCAATGACTAGTC
 CTCATCCATGTAGCACCCTAATCTTCCATGCTGGAGAAACCTGGGACTTAGTTAGGTAGATTAATATCT
 GGAGCTCTCGAGGGACCAAACTTCCAACCTTTTTTCCOCTCACTAGCACCTGGAATGATGCTTTGTATGTGG
 CAGATAAGTAAATTTGGCATGCTTATATATTCTACATCTGTAAAGTGTGAGTTTATGGAGAGAGCCCTTTT
 ATGCTTAATTTGTCATATGGCAATTAATCCAGAAGGATCTGTAGATGAGGCACCTGCTTTTCTTTCTCTC
 ATTGTCACCTTACTTAAAGTCAGTAGATCTTACCTCATAACTCTCTCCAAAGGCAGCTCAGAAGATTAG
 AACCGACTTACTAACCCTTCCACCCCAACCAACCCCTTCTACTGCGCTCTTTAAAAAATTAATAGTTTT
 CIATGGAAGTATCTAAGATTAGAAAAATTAATTTCTTTAATTTCAATTGACCTTTTATTTACATGACTCTA
 AGACTATAAGAAAATCTGATGGCACTGACAAAGTGTAGCATTTATTTGTTCTAATAAGAACTTGAAGCATA
 TGTGCACTTATGAGTGTATCAGTTGTTGCAATGTAATTTTTGCCTTTGTTTAAAGCTGGAACCTGTGAAGAAAT
 GAAAAATTAATTTTCTTAGGACGAGCTATAGAAAAGCTATGAGAGTATCTAGTTAATCAGTGACAGTAGT
 TGGAAACCTTGTGGGTGTATGTATGTCTGTCTTTGAATGACTTTATCATCTAGTCTTTGTCTATTT
 TCCCTTGATGTTCAAGTCTAGTCTATAGGATTGGCAGTTTAAATGCTTTACTCCCTTTTAAAAATAATGAT
 TAAATGTGCTTTGAAAAAAGAAAAAAGAAAAAAGAAAAA

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MRPGLSFLLLALLFFLGLQAAGDLGDVGPPIPSPGFSSFPGVDSSSSSFSSSSRSGSSSSRSLGS
GGSVSQLFSNFTGSVDGRGCQCSVSLPDTHFPVDRVERLETAHVLSQKFEKELSKVREYV
QLISVYEKKLLNLTVRIDIMEKDTISYTELDFELIKVEVKEMEKLVIQLKESFGSGSEIVDQ
LEVEIRNMNTLLVEKLETLDKNNVLAIRREIVALTKLKECEASKDQNTPVVHPPPTPGSCGH
GGVVNISKPVSQVLNRWGFSYLGAWGRDYSPQHNPGLYWVAPLNITDGRLLLEYRYLNTLD
DLLLYINARELRITYQGSGTAVYNNMVMYNTGNIARVNLTTNTIATQTLPNAAYNNR
FSYANVAWQDIDFAVDENGLWVIYSTAEGNMVISKLNDDTLQVLNTWYTKQYKPSASNAF
MVCGLVYATRMTNTRTEEIFFYYDTNTGKEGKLDIVMHKMQEKVQSINYNPFDQKLYVYNDG
YLLNYDLSVLQKPO

FIGURE 39

GCTCTGAAGACCAAGCTGAAAGAGTGTGAGGCCCTCTAAAGATCAAACACCCCTGTCGTCCAC
CCTCCTCCCACCTCCAGGGAGCTGTGGTCATGGTGGTGTGGTGAACATCAGCAAACCGTCTGT
GGTTCAGCTCAACTGGAGAGGGTTTTCTTATCTATATGGTGCTTGGGGTAGGGATTACTCTC
CCCAGCATCCAAACAAAGGNATGTATTGGNGGCCATTGAATACAGATGGGAGACTGTTG
GAGTATTATAGACTGTACAACCCACTGGATGATTGCTATTGTATATAAATGCTCGAGAGTT
GCGGATCACCTATGGCCAAGGTAGTGGTACAGCAGTTTACAACAACAACATGTACGTCAACA
TGTACAACACCGGNATATTGCCAGAGTTAACCTGACC

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FIGURE 40

TCTCGCAGATAGTAAATAATCTCGGAAAGGCAGAAAGAAGCTGTCTCCATCTTGTCTGTAT
 CGGCTGCTCTTGTGACGTTGTGGAGATGCGGGAGCGTCTGGGGCTGTGCTCCATGGCGAGCT
 GGAATACCATTGTTTGTGGAAAGTGCCTCGTGTGGCTATGCCGATGCTGTCCATGGGAAAC
 AACTCCACTGTAACTAGATTGATCTATGCACTTTTCTTGCTTGTGGAGTATGTTGAGCTTG
 TGTAAATGTGATACCAGGAATGGAAGAACAACTGAATAAGATTCTCGGATTTTGTGAGAAATG
 AGAAAGGTGTTGTCCCTTGTAACTTTTGGTTGGCTATAAAGCTGTATATCGTTTGTGCTTT
 GGTTTGGCTATGTTCTATCTTTCTCTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGA
 TCCTAGAGCTGCAGTGCACAATGGATTTTGGTTCTTTAAATTTGCTGCAGCAATTGC AATTA
 TTATTGGGGCATTCTTCATTCAGAAAGGAACTTTACAACGTGTGGTTTTATGTAGGCATG
 GCAGGTGCCTTTTGTTTCATCTCATACAACCTAGTCTTACTTATTGATTTTGCACATTCATG
 GAATGAATCGTGGGTTGAAAAAATGGAAGAAAGGGAACCTCGAGATGTTGGTATGCAAGCTTGT
 TATCAGCTACAGCTCTGAATTATCTGCTGTCTTTAGTTGCTATCGTCCCTGTTCTTTGTCTAC
 TACACTCATCCAGCCAGTTGTTCCAGAAAAAGGCGTTTCATCAGTGTCAACATGCTCCTCTG
 CGTTGGTGCTTCTGTAATGTCTATACCTGCAAAAAATCCAAGAATCACAACCAAGATCTGGTT
 TGTTCACAGTCTTCAGTAATTACAGTCTACACAATGTATTTGACATGGTCAGCTATGACCAAT
 GAACCAGAAAAAAATTCGAACCAAGTCTACTAAGCATAATTTGGCTACAATACAACAAGCAC
 TGTCCCAAGGAAGGGCAGTCAGTCCAGTGGTGGCATGCTCAAGGAATTATAGGACTAATTC
 TCTTTTGTGTTGTGATTTTATTCAGCATCCGTACTTCAACAATAGTCAGGTTAATAAA
 CTGACTCTAACAAGTGAATGAATCTACATTAATAGAAGATGGTGGAGCTAGAAGTGTGGATG
 ACTGGAGGATGGGGCAGATGTTCAACGAGCTGTAGATAATGAAAGGATGGTGTCACTTACA
 GTTATTGCTCTTTTCACTCATGCTTTTCTGGCTTCACTTTATATCATGATGACCCCTTACC
 AACTGGTCCAGGTATGAACCCCTCTGTTGAGATGAAAGTCAAGTGGACAGCTGTCTGGGTGAA
 AATCTCTCCAGTTGGATTTGGCATCGTGTGATGTTTGGACACTCGTGGCACCACTTGTGTC
 TTACAAATCGTGATTTTGACTGAGTGTGAGACTTCTAGCATGAAAGTCCCACCTTTGATATTGCT
 TTATTTGAAACAGTATTTCCCAACTTTGTAAAGTTGTGATGTTTTTGTCTCCCATGTAAC
 TTCTCCAGTGTTCTGGCATGAATTAGATTTTACTGCTTGTGATTTTGTATTTTCTTACCAA
 GTGCATGTGATGTGAAGTGAATGAATTCAGAGGAAAGTTTATGAATATGGTGATGAGT
 TAGTAAAGATGGCCATTATTTGGGCTTATCTCTGCTCTATAGTTGTGAAATGAAGAGTAAAA
 ACAAAATTTGTTTGACTATTTTAAAAATATATTAGACCTTAAGCTGTTTTAGCAAGCATTA
 GCAAAATGTATGGCTGCCTTTTGAAATATTTGATGTGTTGCCCTGGCAGGATACTGCAAGAAC
 ATGGTTTTATTTAAAAATTTATAAACAGTCACTTAAATGCCAGTTGTCTGAAAAATCTTATA
 AGGTTTTTACCCTTGATACGGAATTTACACAGGTAGGGAGTGTTTAGTGGCAATAGTGTAGG
 TTATGGATGGAGGTGTCGGTACTAAATTTGAATAACAGGTAAATAATCTTACTTGGGTAGAGA
 TGGCCTTTGCCAACAAAGTGAACCTGTTTGGTTGTTTTAAACTCATGAAGTATGGGTTCACT
 GGAATGTTTGGAACTCTGAAGGATTTAGACAAGGTTTTGAAAAGGATAATCATGGGTTAGA
 AGGAAGTGTTTGAAAGTCACTTTGAAAGTGTAGTTTGGGCCAGCAGCGTAGCTCACCCCTT
 GGTAAATCCGAGCACTTTGGGAGCTTAAGTGGGTAGATTACTTGAGCCAGGAATTCAGACCA
 GCTTTGGCACAATGGTGAACCTGTTCTATAAAAAATAATCTGGCTTTGAGCATATGCTCTGGTCT
 CAGCACTGAGAGGCTAGTGAAGATTGCTGAGCCAGAGCCAAAGGTTGCAAGTGAAGAGTCA
 CGTCACTGCATCTAGCTGGCAGAGTAAAGCCAAAAAATATATATATTTGAAATCAAGG
 AGGCAAAATTTTACAGGGAAGGAAGTAACTGCAAAACCACTAGGCTTTAGTAGGCTACTTAT
 ATAAAACTAGTCCAGTTCTCTCATTAAAAAATGAAGACACTGAAATACAGACTTAAATA
 GCTCAGATAGCTAAATAGGAATTTCAAGTTGGCCAAATATAGCATCTCTCTGACATTTTAA
 AATAAATTTCTATTCAAAATACATGCATATTGATTTACACCTCATACTGTGATAAATTAATGT
 TGTGATGATGCTGGTGTCCAGCATGACCCATAACAGGTGAGAAAGTGAAGTATGGAATGTTTT
 AGAATAAATCCTGCTTATAGTATACACAGTTCAAAAGATGTTTAAATGCTTTTGTAT
 TTACTGCCATGTAAATGAATAATATAGATTATTGTAACCTTTCAACCTGAAATCAAGCAGT
 ATGAGAGTTTGTATTTGTATGTGCTAGTGTCTAATGAGCTTTTAAATCTCAACAT
 TCTCTTTTAAAAATTTTATTAATGTGAATGGAATATAACAACTCAGCTTAATTTCCCAACC
 TTATCTGTGTGATGACATTTGTATTCACAATTTTGAATGGCTGTGTTTTACCTCTAAATAA
 ATGAATTCAGAGAAAAA

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FIGURE 41

MGSVLGLCSMASWIPCLCGSAPCLLCRCCPSGNNSTVTRLIYALFLLVGVCVACVMLIPGME
EQLNKIPGFCENEKGVVPCNILVGKAVYRLCFGLAMFYLLSLLMIKVKSSSDPRAAVHNG
FWFFKFAAAIAIIIGAFFIPEGTFTTVWFYVGMAGAFCFILIQVLVIDFAHSWNESWVEKM
EEGNSRCWYAALLSATALNYLLSLVAIVLFFVYTHPASCSENKAFISVNMLLCVGASVMSI
LPKIQESQPRSGLLQSSVITVYTMYLTSAMTNEPETNCNPSLLSIIGYNTTSTVPKEGQSV
QWWHAQGIIGLILFLLCVFYSSIRTSNNSQVNKLTLTSDESTLIEDGGARSDGSLEDGDDVH
RAVDNERDGVTSYSFFHFMLFLASLYIMMTLTNWSRYEPSREMKSQWTAVVWKISSSWIGI
VLYVWTLVAPLVLNDRFD

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FIGURE 42

GCGAGAAAGAAGCTGTCTCCATCTTGTCTGTATCCCCTGCTTCTTGNGACGTTGTGGAGAT
GGGGAGCGTCCCTGGGGCTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAGTGCC
CCGTGTTTGTCTATGCCGATGCTGTCCTAGTGGAACAANTCCACTGTAAC TAGATTGATCTA
TGCACTTTTCTTGCTTGTGGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAG
AACAACTGAATAAGATTCTGGATTTTGTGAGAATGAGAAAGGTGTTGTCCCTTGTAACATT
TTGGTTGGCTATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTTCT
CTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGAT
TTTGGTTCTTTAAATTGCTGCAGCAATTGCAATTATTATTGGGGC

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FIGURE 43

GTTATTGTGAACTTTGTGGAGATGGGAGGTCNTGGGGCTGTGTTCCATGGCGAGCTGGATAC
CANGTTTGTGTGGAAGTGCCCGTGTGTTGNTATGCCGATGCTGTCCTAGTGGAACAANTCC
ACTGTAATTAGATTGATNTATGCACTTTTNTTGCTTGTGGAGTANGTGTAGCTTGTGTAAT
GTTGATACCAGGAATGGAAGAACAACTGAATAAGATTCTGGATTTTGTGAGAATGAGAAAG
GTGTTGTCCTTGTAAACATTTGGTTGGCTATAAAGCTGTATATNGTTTGTGCTTTGGTTTG
GCTANGTTCTATNTTCTTCTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAG
AGCTGCAGTGACAATGGATTTTGTTTTTAAATTTGCTGCAGCAATTGCAATTATTATTG
GGGC

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AAGAAGCTGTCTCCATCTTGTCTGTATCCGCTGCTCTTGTGAACGTTNTGGAGATGGGGAGC
GTCCTTGGGGTTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAGTGCCCCGTGTT
TGCTATGCCGATGCTGTCTAGTGGAACAACCTCCACTGTAAGTATGATTGATCTATGCACTT
TTCTTGCTTGTGGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAGAACAAC
GAATAAGATTCTGGATTTTGTGAGAATGAGAAAGGTGTTGCCCTGTAACATTTTGGTTG
GCTATAAAGCTGTATATCGTTTGTGCTTGGTTTGGCTATGTTCTATCTTCTCTCTTTA
CTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGATTTTGGTT
CTTTAAATTGCTGCAGCAATTGCAATTATTATGGGGC

FIGURE 45

GCTGTCCTTAGTGGAACAANTCCAACCTTGTAACCTTGGATTGATCTATGCACTTTTTCCTTG
CTTGTTGGAGTATGTGTAGCTTTGTGTAATGTTGTTCCCAGGATTGGANGAACAACTGAATA
AGATTCCCTGGATTTTTGTGAGAATGAGAAAGGTGTTGTCCCCTTGTAACATTTTTGGTTGGC
TATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTCTCTCTTTACT
AATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGATTTTGGTTCT
TTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGCATTCTTCATTCCAGAAGGAACTTTT
ACAACTGTGTGGTTTTATGTAGGCATGGCAGGTGCCTTTTGTTTCATCCTCATACAACTAGT
CTTACTTATTGATTTTGCACATTCATGGAATGAATCGTGGGTGAAAAATGGAAGAAGGGA
ACTCGAGATGTTGGTATGCAGCCTTGTTATCAGCTACAGCTCTGAATTATCTGCTGTCTTTA
GTTGCTATCGTCCTGTTCTTTGTCTACTACACTCATCCAGCCAGTTGTTGAGAAAACAAGGC
GTTTCATCAGTGTCACATGCTCCTCTGCGTTGGTGCTTCTGTAATG

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[illegible]

MGPPSLVLCLLSATVFSLLGGSSAFLSHRLKGRFQRDRNRNIRPNIILVLTDDQDVELGSMQ
VMNKTRRIMEQGGAHFVINAFTVTPMCCPSRSSILTKYVHNHNTYTNNENCSSPSWQAQHE
RTFAVYLNSTGYRTAFFGKYLNEYNGSYVPPGWKEWGLLKNRFRNYTLCRNGVKEKHGSD
YSKDYLTLTITNDSVSFFRTSKKMYPHRPVLMVISHAAPHGEDSAQYSRLFNPASQHITP
SYNYAPNPKHWMIRYTGPMKPIHMEFTNMLQRKRLQTLMSVDDSMETIYNMLVETGELDNT
YIVYTADHGXYHIGQFGLVKGKSMPEYFDIRVPFYVRGPNVEAGCLNPHIVLNI DLAPTILDI
AGLDIPADM DGKSILKLLDTERPVNRFHLKKKMRVWRDSFLVERGKLLHKRDN DKVDAQEEN
FLPKYQRVKDLCQRAEYQTACEQLGQKWQCVEDATGKGLHKHCKGPMRLGGSRALSNLVPKY
YGGGSEACTCDSDGYKLSLAGRRKKLFKKKYKASYVRSRSIRSAIEVDGRVYHVGLGDAQ
PRNLTKRHWPGAPEDQDDKDGGDFSGTGGLPDYSAANPIKVTHRCYILENTVQCDL DLYKS
LQAAWKDHLKHLIDHEIETLQNKIKNLRVGRHKLKKRKEPEECDCHCISYTHQHKRGLKHRGSSL
HFFARKGLQEKDKVWLLRQEKRRKKLRLKRLKRLNNDTCSMPGLTXYTHDNQHWQTAPFWTLG
PFCACTSANNTYIMREQTINETHNLFLCEFATGFLEYFDLNTDPYQLMNAVNTLDRDVLNQL
HVQLMELRSCKGYKQCNPRTRNMDLDGGSYEQYRQFQRRKWPEMKRPSKSLGQLWEGWEG

FIGURE 48

AACAAAGTTCAGTGACTGAGAGGGCTGAGCGGAGGCTGCTGAAGGGGAGAAAGGAGTGAGGA
GCTGCTGGGCAGAGAGGGACTGTCCGGCTCCCAGATGCTGGGCCTCCTGGGGAGCACAGCCC
TCGTGGGATGGATCACAGGTGCTGCTGTGGCGGTCTGCTGCTGCTGCTGCTGCTGGCCACC
TGCCTTTTCCACGGACGGCAGGACTGTGACGTGGAGAGGAACCGTACAGCTGCAGGGGGAAA
CCGAGTCCGCCGGGCCAGCCTTGCCCTTCCGGCGGCGGGGCCACCTGGGAATCTTTCACC
ATCACCGTCATCCTGGCCACGTATCTCATGTGCCGAATGTGGGCTCCACCACCACCACCAC
CCCCGCCACACCCCTCACCACCTCCACCACCACCACCACCCACCAGCCACCATCCCCGCCA
CGCTCGCTGAAGGCTGCTGTGCGCGGTGCCTGTGGACAGCAGCTGCCCTGCCCTCCCATCTG
TTCCAGGACAAGTGACCCCATGTTTCCATGTGGAAGGATGCATCTCTGGGGTGAACGAGG
GGAACAATAGACTGGGGCTTGCTCCAGCTGCATTTGCATGGCATGCCCCAGTGACTATGGC
AGCAGAGAATGGAGGAACACTGGGTCTGCACTGCTGAAGGGTTTGGGGAGTGGAGAGCAAGG
GTGCTCTTTCGGGGCTGGACAGCCGCTTGTGACAGTGACTCCAGTGAGCCCCAGAAATG
ACAAGCGTGTCTTGGCAGAGCCAGCACACAAGTGGATGTGAAGTGCCCGTCTTGACCTCCTC
ATCAGGCTGCTGCAGGCCTCTGGCGGGCAGGGCACTGGGAGAGGCCCTGAGAATGTCCTTTT
GGTTTGAGAAGGCAGTGTGAGGCTGCACAGTCAATTATCGGTGCCTTAGTCCAAGAAAAT
AAAAACCACTAAGAAGCTTTAAAAAAAAAAAAAAAAAAAAA

FIGURE 49

MLGLLGSTALVGWITGA AVAVLLLLLLLATCLFHGRQDCDVERNRTAAGGNRVRAQPWPFR
RRGHLGIFHHHRHPGHVSHVPNVGLHHHHHPRHTPHHLHHHHHPHRRHPRHAR

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GGCGGCTGCTGAGCTGCCTTGAGGTGCAGTGTGGGGATCCAGAGCCATGTCGGACCTGCTA
CTACTGGGCTGATTGGGGGCTGACTCTCTTACTGCTGCTGACGCTGCTGGCCTTTGCCGG
GTA CT CAGGGCTACTGGCTGGGGTGAAGTGAGTGCTGGGTACCCCCCATCCGCAACGTCA
CTGTGGCCTACAAGTTCACATGGGGCTCTATGTTGAGACTGGGCGGCTTTTCTACTGAGAG
TGCAGCATCTCTCCCAAGCTCCGCTCCATCGCTGTCTACTATGACAACCCCCACATGTTGCC
CCCTGATAAGTGCCGATGTGCCGTGGGCAGCATCCTGAGTGAAGGTGAGGAATCGCCCTCCC
CTGAGCTCATCGACCTCTACCAGAAATTTGGCTTCAAGGTGTTCTCCTTCCCGGCACCCAG
CATGTGGTGACAGCCACCTTCCCCTACACCACCATCTGTCCATCTGGCTGGCTACCCGCCG
TGTCCATCTGCCTTGGACCTACATCAAGGACGGAAGCTGTGTGCCCTACTCGCTGGTGG
AGATCTACCAGGAAGACAGATGCATTTCATGTGCCCATGGCAGCGCAGGGAGACTTCTAT
GTGCCTGAGATGAAGGAGACAGAGTGGAAATGGCGGGGGCTTGTGGAGGCCATTGACACCCA
GGTGGATGGCACAGGAGCTGACACAATGAGTGACACGAGTTCTGTAAGCTTGGAAAGTGAGCC
CTGGCAGCCGGGAGACTTCAGCTGCCACACTGTCACTGGGGCGAGCAGCCGTGGCTGGGAT
GACGGTGACACCCGACGCGAGCACAGCTACACGAGTCAGGTGCCAGCGGCTCCTCTTTTGA
GGAGCTGGACTTGGAGGGCGAGGGGCCCTTAGGGGAGTCACGGCTGGAACCTGGGACTGAGC
CCCTGGGGACTACCAAGTGGCTCTGGGAGCCCACTGCCCTGAGAAGGGCAAGGAGTAACCC
ATGGCTGACCCCTCCTGCAGTGCAAGTGTGCTGAGGAAGTGAGCAGACTCTCCAGCAGACTCT
CCAGCCCTCTTCTCCTTCTCTGGGGGAGGAGGGGTTCTGAGGGACCTGACTTCCCTTGC
TCCAGGCCTCTTGCTAAGCCTTCTCCTCACTGCCCTTTAGGCTCCCAGGGCCAGAGGAGCCA
GGGACTGATTTCTGCACACGCCCCAGGGCTGCCGCCCTGTTGTGTCTTTTTTTCAGACTA
ACAGTGGAGCTTCCAGGACCCAGAATAAGGCCAATGATTACTTGTGTTACCTGGAAAAAA
AAAAA

FIGURE 51

MSDLLLGLIGGLTLLLLLTLAFAGYSGLLAGVEVSAGSPPIRNVTVAYKFHMGlyGETGR
LFTESCSISPKLRSIAVYYDNPHMVPPDKRCRAVGSI LSEGEESPSPELIDLYQKFGKVF S
FPAPSHVVTATFPYTTILSIWLATR RVHPALD TYIKERKLCAYPRLEIYQEDQIHFMCP LAR
QGDFYVPEMKETEWKWRGLVEAIDTQVDGTGADTMSDTSSVSLEVSPGSR ETSAA TLSPGAS
SRGWDDGDTRSEHSYSESGASGSSFEELDLEGE GPLGESRLDPGTEPLGTTKWLWEPTAPEK
GKE

FIGURE 52

CCGCGGGAACGCTGTCCTGGCTGCCGCCACCCGAACAGCCTGTCCTGGTGCCCCGGCTCCCT
GCCCCGCGCCAGTCATGACCCTGCGCCCTCACTCCTCCCGCTCCATCTGCTGCTGCTGCT
GCTGCTCAGTGCGGCGGTGTGCCGGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGA
CCCTCCAAGTGGAGACCCTGGTGGAGCCCCCAGAACCATGTGCCGAGCCCGCTGCTTTGGA
GACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCT
GACCAGAGACCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGA
GTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCCTTCTCACTTGGCCTAT
GGAAAACGGGGATTTCACCATCTGTCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCT
GATTGCACTAATCCGAGCCAACTACTGGCTAAAGCTGGTGAAGGGCATTTCCTCTGGTAG
GGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTTGGGTATCACCTATACAGAAAGCCAAT
AGACCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAAGAAATTA
ATAAATAATAAATTTTAAAAAACTTAAAAAAAAAAAAAAAAAA

FIGURE 53

MTLRPSLLPLHLLLLLLLLSAAVCRAEAGLETESPVRTLQVETLVEPPEPCAEPAAFGDTLHI
HYTGSLVDGRIIDTSLTRDPLVIELGQKQVIPGLEQSLLDMCVGEKRRAIIPSHLAYGKRGF
PPSVPADAVVQYDVELIALIRANYWLKLVKILPLVGMAMVPALLGLIGYHLYRKANRPKVS
KKKLKEEKRNSKKK

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FIGURE 54

CCCGGGAACGTGTTCTGCTGCCGCACCCGAACAGCCTGTCCTGGTGCCCCGGCTCCCTGC
CCCGCGCCAGTCATGACCCTGCGCCCCCTCACTCCTCCCGCTCCATCTGCTGCTGCTGCTGC
TGCTCAGTGCGGCGGTGTGCCGGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGACC
CTCCAAGTGAGACCCTGGTGGAGCCCCCAGAACCATGTGCCGAGCCCGCTGCTTTTGGAGA
CACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCTGA
CCAGAGACCCTCTGGTTATAGAACTTGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGAGT
CTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCTTCTCACTTGCCCTATGG
AAAACGGGGATTTCCACCATCTGTCCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCTGA
TTGCTACTAATCCGAGCCAACTACTGGCTAAAGCTGGTGAAGGGCATTTTGCCTCTGGTAGGG
ATGGCCATGTTGCCACCCTCCTGGGCCTCATTGGGTATCACCTATACAGAAAGGCCAATAGA
CCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAAGAAATAATA
AATAATAAATTTTAAAAAAGCTTA

FIGURE 55

CCGAAAGTCCCGTCCGGACCCCTCCAAGTGGAGACCCCTGGTGGAGCCCCAGAACCATGTGCC
GAGCCCGCTGCTTTTGGAGACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACG
TATTATTGACACCTCCCTGACCAGAGACCCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGA
TTCCAGGTCTGGAGCAGAGTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATT
CCTTCTCACTTGGCCTATGGAAAACGGGGATTTCCACCATCTGTCCAGCGGATGCAGTGGT
GCAGTATGACGTGGAGCTGATTGCACTAATCCGAGCCAACACTACTGGCTAAAGCTGGTGAAGG
GCATTTTGCCTCTGGTAGGGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTGGGTATCAC
CTATACAGAAAGGCCAATAGACCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAA
CAAGAGCAAAAAGAAATAATAATAATAAATTTAAAAAACTTAAAA

TATTATTGACACCTCCCTGACCAGAGACCCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGA

FIGURE 56

CTGCTGCATCCGGGTGTCTGGAGGCTGTGGCCGTTTTGTTTTCTTGGCTAAAATCGGGGAG
 TGAGGCGGGCGCGCGCGCGACACCGGGCTCCGGAACCACTGCACGACGGGGCTGGACTG
 ACCTGAAAAAAATGTCCTGGATTCTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGG
 GAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGTACTATTTTTTACAGGCTGGTGGAT
 TATCATAGATGCAGCTGTTATTTATCCCACCATGAAAGATTTCAACCACTCATACCATGCCT
 GTGGTGTATAGCAACCATAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGA
 GGTGATAGTTACAGTGAAGGTTGTCTGGGTCAAACAGGTGCTCGCATTGGCTTTTCGTTGG
 TTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTGGAGGTTATGTTG
 CTAAAGAAAAAGACATAGTATACCCTGGAATTGCTGTATTTTCCAGAATGCCTTCATCTTT
 TTTGGAGGGCTGGTTTTTAAGTTTGGCCGCACTGAAGACTTATGGCAGTGAACACATCTGAT
 TTCCACAGCACAAACAGCCCTGCATGGGTTGTTTGTTTTTTACIGCTCACTCCCAACCTT
 TTGTAATGCCATTTTCTAACTTATTTCTGAGTGTAGTCTCAGCTTAAAGTTGTGTAATACT
 AAAATCACGAGAACCTTAAACAACAACCAAAAATCTATTGTGGTATGCACCTTGATTAACCT
 ATAAATGTTAGAGGAACTTTCACATGAATAATTTTTGTCAAATTTTATCATGGTATAATT
 TGTAAAAATAAAAAGAAATTACAAAAGAAATTATGGATTGTCAATGTAAGTATTTGTCATA
 TCTGAGGTCCAAAACCACAATGAAAGTGCTCTGAAGATTTAATGTGTTTATTCAAATGTGGT
 CTCTTCTGTGTCAAATGTTAAATGAAATATAAACATTTTTTAGTTTTTAAATATTCCGTGG
 TCAAAATCTTCTCACTATAATTGGTATTACTTTTACCAAAAATCTGTGAACATGTAAT
 GTAACTGGCTTTTGAGGGTCTCCCAAGGGGTGAGTGGACGTGTTGGAAGAGAGAAGCACCAT
 GGTCCAGCCACCAGGCTCCCTGTGTCCCTTCCATGGGAAGGTCTTCCGCTGTGCCTCTCATT
 CCAAGGCAGGAAGATGTGACTCAGCCATGACACGTGGTTCTGGTGGGATGCACAGTCACTC
 CACATCCACCACTG

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FIGURE 57

MSGFLEGLRCSECIDWGEKRNTIASIAAGVLFFTGWWIIIDAAYPTMKDFNHSYHACGVI
ATIAFLMINAVSNGQVRGDSYSEGCLGQTGARIWLFVGFMLAFGSLIASMWILFGGYVAKEK
DIVYPGIAVFFQNAFIFFGGLVFKFGRTEDLWQ

0090440.11401

FIGURE 58

TTCTTGGCTAAAATCGGGGGAGTGAGGCGGGCCGGCGCGCGACACCGGGCTCCGGAACC
ACTGCACGACGGGGCTGGACTGACCTGAAAAAATGTCTGGATTCTAGAGGGCTTGAGATG
CTCAGAATGCATTGACTGGGGGAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGTAC
TATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGTTATTTATCCCACCATGAAAGAT
TTCAACCACTCATACCATGCCTGTGGTGTTATAGCAACCATAGCCTTCCTAATGATTAATGC
AGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTGTCTGGGTCAAACAGGTG
CTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTGGATCTCTGATTGCATCTATGTGG
ATTCTTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAGTATACCCTGGAATTGCTGTATT
TTTCAGAATGCCITTCATCTTTTTTGGAGGGCTGGTTTTTAAGTTTGGC

09060401-0440660

FIGURE 59

TGGACGGACCTGAAAAAATGTTTGGATTNTAGAGGNTTGAGATGTTTCAGAATGCATGAC
TGGGGGAAAAGCGCAAATACTATTGCTTCCATTGCTGCTGGTGTANTATTTTTTACAGGCTG
GTGGATTATCATAGATGCAGNTGTTATTTATCCCACCATGAAAGATTTCAACCANTCATACC
ATGCCTGTGGTGTTATAGCAACCATAGCCTTCNTAATGATTAATGCAGTATCGAATGGACAA
GTCCGAGGTGATAGTTACAGTGAAGGTTGTTTGGGTCAAACAGGTGCTCGCATTGGCCTTTT
CGTTGGTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTGGAGGTT
ATGTTGCTAAAGAAAAAGACATAGTATACCCTGGAATTGNTGTATTTTCCAGAATGCCTTC
ATCTTTTTTGGAGGGCTGGTTTTTAAGTTTGGCCGCACTGAAGANTTATGGCAGTG

009900.1144

FIGURE 60

GGACACCGGGTCCGGACCAATGCANGACGGGTGGANTGACCTGAAAAAATGTTTGGATT
TTTAGAGGGCTTGAGATGNTCAGAATGCATTGACTGGGGGAAAAGCGCAATANTATTGCTTT
CCATTGCTGCTGGTGTACTATTTTTTACAGGGTGGTGGATTATCATAGATGCAGCTGTTATT
TATCCCACCATGAAAGATTTNAACCACTCATACCATGCCTGTGGTGTTATAGCAACCATAGC
CTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTT
GTTTGGGTCAAACAGGTGNTCGCATTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGGATTT
CTGATTGNATTCTATGCGGATTCTTCTGGAGGTTATGTTGCTAAAGAAAAAGACATAGTAT
ACCCTGGAATTNCTNTATTTTCCAGAATGCC

090944 1140

FIGURE 61

TAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGAAAAGCGCAATANTATTGCTTCC
ATTGNTGNTGGTGTANTATTTTTTTACAGGCTGGTGGATTATNATAGATGCAGCTGTTATTT
ATCCCACCATGAAAGATTTNAACCANTCATACCATGCCCTGTGGTGTTATAGCAACCATAGCC
TTCTTAATGATTAATGCAGTATNGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTG
TTTGGGTCAAACAGGTGNTNGCATTGGCTTTTNGTTGGTTTCATGTTGGCCTTTGGATCTN
TGATTGCATTATGTGGATTNTTTTTGGAGGTTATGTTGCTAAAGNAAAAGACATAGTATAC
CCTGT

TCTTT: 040660

FIGURE 62

GGGAGGCTGTGNCCGTTTTGTNTTGGCTAAAATCGGGGAGTGAGGCGGCCCGCGCGG
CGNGACACCGGGTCCGGGAACCATTCACGACGGGGTGGACTGACCTGAAAAAATGTTTG
GATTTNTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGAAAAGCGCAATACTATT
GCTTCCATTGCTGCTGGTGTACTATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGT
TATTTATCCCACCATGAAAGATTTCAACCACTCATACCATGCCTGTGGTGTTATAGCAACCA
TAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAA
GGTTGCTCTGGGTCAAACAGGTGCTCGCATTTGGCTTTTCGTTGGTTTCATGTTGCCCTTTGG
ATNTCTGATTGCATCTATGTGGATTCTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAG
TATACCTGGAATTGCTGTATTTTCCAGAATGCCTTCATNTTTTTTGGAGGGCTG

0990049-11441

[illegible]

FIGURE 64

MWLPLVLLLAVALLLAVLCKVYLGLEFSGSSPNPFSESVKRPAPLVTDKEARKKVLKQAFSAN
QVPEKLDVVVIGSGFGGLAAAAIILAKAGKRVLVLEQHTKAGGCCHTFGKNGLEFDTGIHYIG
RMEEGSIGRFILDQITEGQLDWAPLSSPFDIMVLEGPNRKEYPMYSGEKAYIQGLKEKFPQ
EEAIIIDKYIKLVKVSSGAPHAILLKFLPLPVVQLLDRCGLLTRFSPFLQASTQSLAEVLIQQ
LGASSELQAVLSYIFPTYGVTPNHSAFSMHALLVNHYMKGGFYPRGGSSEIAFH TIPVIQRA
GGAVLTATVQSVLLDSAGKACGVSVKKGHELVNIYCPIVVSNAGLFNTYEHLLPGNARCLP
GVKQQLGTVRPGGMTSVFICLRGTEKEDLHLPSTNYYVYYDTDMDQAMERYVSMPREAAEH
IPLFFAFPSAKDPTWEDRFPRSTMIIMLIPTAYEWFEEWQAEKKGKRGSDYETFKNSFVEA
SMSVVLKLFQLEGKVESVTAGSPLTNQFYLAAPRGACYGADHDLGRLHPCVMASLRAQSPI
PNLYLTGQDIFTGCLVGALQGALLCSSAILKRNLYSDLKNLDSRIRAQKKKN

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[illegible]

MRVRIGLTLLLCVALLSLASASSDDEEGSQDESLSKTTLTSDSESVKDHTTAGRVVAGQIFLD
SESELESSIQEEDSLKSQEGESVTEDTSFLESPNPENKDYEEPKKVRKPAITAIEGTAHG
EPCHFPFLFLDKYDECTSDGREDGRLWCATTYDYKADEKWFGEETEEAAKRRQMQEAMM
YQTGMKILINGSNKKSQKREAYRYLQKASMNHTKALERVSYALLFGDYLPQNIQAREMEFK
LTGEGSPKQGTALGFLYASGLGVNSQKALVYTYFGALGGNLIAMVLVSRSL

FIGURE 67

CTTCCCAGCCCTGTGCCCCAAAGCACCTGGAGCATATAGCCTTGCAGAACTTCTACTTGCCT
GCCTCCCTGCCTCTGGCCATGGCCTGCCGGTGCCTCAGCTTCCTTCTGATGGGGACCTTCCT
GTCAGTTTCCCAGACAGTCCCTGGCCCAGCTGGATGCACTGCTGGTCTTCCCAGGCCAAGTGG
CTCAACTCTCCTGCACGCTCAGCCCCCAGCACGTCACCATCAGGGACTACGGTGTGTCTGG
TACCAGCAGCGGGCAGGCAGTGCCCCCTCGATATCTCCTCTACTACCGCTCGGAGGAGGATCA
CCACCGGCCTGCTGACATCCCCGATCGATTCTCGGCAGCCAAGGATGAGGCCCAATGCCT
GTGTCTCACCATTAGTCCCGTGCAGCCTGAAGACGACGCGGATTACTACTGCTCTGTTGGC
TACGGCTTTAGTCCCTAGGGGTGGGGTGTGAGATGGGTGCCTCCCCTCTGCCTCCCATTCT
GCCCCTGACCTTGGGTCCCTTTTAAACTTTCTCTGAGCCTTGCTTCCCCTCTGTAAATGGG
TTAATAATATTCAACATGTCAACAAC

CTTCCCAGCCCTGTGCCCCAAAGCACCTGGAGCATATAGCCTTGCAGAACTTCTACTTGCCT

FIGURE 68

MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPQGVAQLSCTLSPQHVTIRDYGVSWYQQRAG
SAPRYLLYYRSEEDHHRPADIPDRFSAKDEAHNACVLTISPVPEDDADYYCSVGYGFSF

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[illegible]

FIGURE 70

MTFSPLLLLLLPLLLLGAFPPAAAAARGPPKMA DKVVPRQVARLGRTVRLQCPVEGDPPPLTM
WTKDGRTIHSGWSRFRVLPQGLKVKQVEREDAGVYVCKATNGFGSLSVNYTLVVLDDISPGK
ESLGPDSSSGGQEDPASQQWARPRFTQPSKMRRRVIA R PVGSSVRLKCVASGHPRPDITWMK
DDQALTRPEAAEPRKKKWTLSLKNLRPEDSGKYTCRVSNRAGAINATYKVDVIQRTRSKPVL
TGTHPVNTTVDFGGTTSFQCKVRSDVKPVIQWLKRVEYGAEGRHNSTIDVGGQKFVVLPTGD
VWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYSFRSAFLT VLPDPKPPGPPVASSSSA
TSLPWVPVIGIPAGAVFILGTLLLWLCQAQKKPCTPAPAPPLPGHRPPGTARDRSGDKDLPS
LAALSAGPGVGLCEEHGS PAAPQHLLGPGPVAGPKLYPKLYTDIHTHTHTSHSHVEGKV
HQHIHYQC

[illegible]

MVVGTKAWVFESFLVLEVTSVLGRQTMLTQSVRRVQPGKKNPSIFAKPADTLESPEGWTTWFNI
DYPGGKGDYERLDAIRFYYGDRVCARPLRLAARTTDWTAGSTGQVHVHSGPREGFWCLNREQ
RPGQNCSNYTVRFLCPPGSLRRDTERIWSFSPWSKCSAACGQTGVQTRTRICLAEMVSLCS
EASEEGQHCMGQDCTACDLTCFPMGQVNADCDACMCQDFMLHGAVSLPGGAFASGAAIYLLT
TPKLLTQTDSGDGRFRIPLGLCPDGKSLIKITKVKFAPIVLTMPKTSLKAATIKAEFVRAETPY
MVMNPETKARRAGQSVSLCCKATGKPRPDKYFWYHNDTLLDPSLYKHESKLVLRKLQHQAG
EYFCKAQSDAGAVKSKVAQLIVTASDETPCNPVPESYILRLPHDCFQONATNSFYDVGRCVP
KTCAGQQDNGIRCDAYQNCGGISKTEIERETQCSGYTLTPTKVAKECSCQRCTETSIRVGRV
SAADNGEPMRFHGVYMGNSRVSMTGYKGTFTLHVPTQTERLVLTFFVDRLQKFVNTTKVLPFN
KKGSAVFHEIKMLRRKEPILEAMEFNIIPLGEVVGEDPMAELEIPRSRIFYRQNGEPEYIGKV
KASVTFLDPRNISTATAAQTDLNFINDEGDTPFLRTYGMFSVDFRDEVTSEPLNAGKVKVHL
DSTQVKMPEHISTVKLWSLNPDTGLWEEEGDFKFENQRRNKRREDRTFLVGNLEIRERRLFNL
DVPESRRCFVKVRAIRSERFLPSEQIQGVVISVINLEPRTGFLSNPRAWGRFDSVITGPGA
CVPAFCDQSPDAYSAYVLASLAGEELQAVESSPKFNPNAIGVPPQYPLNKLNYRRTDHEDPR
VKKTAFAQISMAKPPRNSAEESNGPIYAFENLRACEEAPPSAAHFRFYQIEGDRYDYNTVPFN
EDDPMSTWEDYLAWWPKPMEFRACYIKVKIVGPLEVNVRSRNMGGTHRRTPMGKLYGIRDVRS
TRDRDQPNVSAACLEFKCSGMLYDQDRVDRTLKVPIPGGSCRRASVNPMLGHEHYLVNHLPLAV
NNDTSEYTM LAPDLPLGHNYGIYTVTDQDPRTAKEIALGRCFDGTSDGSSRIMKSNVGVALT
FNCVERQVGRQSAFYQLQSTPAQSPAAGTVQGRVPSRRQRGRVSGGGQRGQGVVNSLRFPRVA
OQPLIN

FIGURE 73

CTGCAAGTTGTTAACGCCATAACACACAAGTATGTTAGGCTTCCACCAAAGTCCTCAATATACCTGAATACGCAC
 AATATCTTAACCTCTTCATATTTGGTTTTGGGATCTGCTTTGAGGTCCCATCTTCATTTAAAAAAAATACAGAG
 ACCTACCTACCCGTCAGCATACATACATATGTGTATATATATGTAACCTAGACAAAGATCGCAGATCATAAAGC
 AAGCTCTGCTTAGTTTCCAAAGAGATTACAAGAATTTAGAGATGTTATTGTCAAGATCCCTGTCGATTCATG
 CCCTTTGGGTTACGGTCTCCTCAGTGATGACGCCCTACCCTTTGGTTGGGGACATTTATGATTGTGTAAGACT
 CAGATTTACACGGAAGAGGAAAGTTTGGGATTACATGGCTGCCAGCCGGAATCCACGGACATGACAAAATA
 TCTGAAGTGAACCTCGATCTCCCGATATTACCTGTGGAGACCTCCTTGAGACGTTCTGTGCAATGGGCAAT
 CCTACATGTGCAATATGAGTGTGATGCGAGTACCCCTGAGCTGGCACACCCCCCTGAGCTGATGTTTGAATTTT
 GAAGGAAGACATCCCTCCACATTTTGGCAGTCTGCCACTTGGAAAGGATATCCCAAGCCTCTCCAGGTTAACAT
 CACTCTGCTTTGGAGCAAAACCATTTAGCTAACAGACAACATAGTTTATACCTTTGAATCTGGGCGTCCAGACC
 AAATGATCTCGGAGAAGTCTCTCGATTATGGACGAACATGGCAGCCCTATCAGTATTATGCCACAGACTGCTTA
 GATGCTTTTCACATGGATCCTAAATCCGTGAAGATTATACAGCATACGGCTCTTGAATCATTTGACACAGA
 AGAGTACTCAACAGGATATACAACAAATAGCAAAATAATCCACTTTGAATCAAAGACAGGTTCCGCTTTTTG
 CTGGACCTCGCCTACGCAATATGGCTTCCCTCTACGGACAGCTGGATACAAACGAAGACTCAGAGATTTCTTT
 ACAGTCAACAGACTGAGGATAAGGCTTTAAGACAGCCGTTGGGGAAATATTTGATGAGTACACTCACTTGGC
 ACGCTACTTTTACGCGATCTCAGACATAAAGGTGCGAGGAAGTTGCAAGTGTAACTCCTCATGCCACTGTATGTG
 TGTATGACAACAGCAAAATGACATGCGAATGTGAGCACAACTACAGGTCAGACTGTGGGAAATGCAAGAG
 AATTATCAGGCGCGACCTTGGAGTCCAGGCTCCTATCTCCCATCCCCAAGGCACTGCAATACCTGTATCCC
 CAGTATTTCCAGTATTTGGTACGAATGTCTGCGACAACAGAGCTCCTGCACTGCCAGACGGAGGACGTGCCACA
 ACAACGTGGCGTGGCTGTGCCGGCGCATACACGGGATCCTCTGCGAGAAGCTGCGGTGCGAGAGGCTGGC
 AGCTGCGGCTCCGACTCTGGCCAGGCGCGCCCCGCGACGGCACCCACGCGTGTCTGCTGTACCCGCTGTCT
 GGGAAACCGCGACCCCTGGTGTCTTGGTGTCACTCCAGCCACACCGGAGGCGCTGTGCGGTGGGGAAGCA
 GACACAACCCAAACATTTGCTACTAATAGGAAACACACATACAGACACCCCACTCAGACAGTGTACAAA
 CTAAGAAGGCTAAGTGAACATAAGCCATATTTATCACCGTGGACAGCACATCCGAGTCAAGACTGTTAATTTT
 TGACTCCAGAGGAGTTGGCAGCTGTTGATATTATCACTGCAATCACAATGCCAGCTGCAGAGCATATTGTGGA
 TTGGAAGGCTGCGACAGCCCCCAACAGGAAGACAAAAACAAACAAATCAACCGACTAAAAACATTGGC
 TACTCTAGCGTGGTGGCGCTTAGTACGACTCCGCCAGTGTCTGGACCAACCAATAGCATTCTTTGCTGTGAG
 GTGCAATTGTGGGATAAGGAATCTGTTACAAAGCTGCCATTGGCCTGCTTCCGTGCTGAATCCCTTCCAAC
 CTGTGCTTTAGTGAACGTTGCTCTGTAACCTCGTTGGTTGAAGATTCTTTGTCTGATGTTAGTGATGCACA
 TGTGTAAACAGCCCTCTAAAGAAGCGCAAGCCAGTCAATACCCCTGTATATCTTAGCAGCACTGAGTCCAGTGGCA
 GCACACCCCACTATAAAGAGTGGCTATAGGAAAAAAGAAAGTGTATCTATCCTTTTGATTCAAATGAAGTT
 ATTTTCTTGAACACTGTAATATGTAGATTTTTGTATTATTGCAATTTGTGTACAGACAACTGTGTTAAT
 GIATCTAATTCGATCAGCAAGACTGACATTTTATTTTGTCTCTTTCGTTCTGTTTTGTTTCACTGTGCGAGA
 GATTTCTCTAGAGGCAACGAACGCTGCTGGCATCAAAGAAATCAGTTTACATATATAAAGAGTGAATAAGA
 TTCACCAAGGCACTTCAAATCTTTCTTGTGCTTTAAACATGGAAAGATTAAAGAAATAAACTCCTGCA
 TAAACGATTTCCAGAAATTTGATTTGCAATTTCTTAAGATGAAGGAACAGCCACCAAGCAGTTTCACTCACT
 TTACTGATTTCTGTGGAGCTGAGTACACTCAGCTGACGAATTTAGTTCCCGAAGAGTGGATTGATGTCTCACT
 AGCTTGGACAACTTCTGCAAAATATGAGACTATTTCCACTTGGGAAAAATACAAACGCAAAAAAATAAAAAA
 AAAAAA

FIGURE 74

MYLSRSLSIHALWVTVSSVMQPYPLVWGHYDLCKTQIYTEEGKVWDYMACQPESTDMTKYLK
VKLDPPDITCGDPPETFCAMGNPYMCNNECDASTPELAHPPELMFDFEGRHPSTFWQSATWK
EYPKPLQVNITLSWSKTIELTDNIVITFESGRPDQMLEKSLDYGRTWQPYQYYATDCLDAF
HMDPKSVKDLSQHTVLEIICTEEYSTGYTTNSKIIHFEIKDRFALFAGPRLRNMASLYGQLD
TTKKLRDFFTVDLRIRLLRPAVGEIFVDELHLARYFYAISDIKVRGRCKCNLHATVCVYDN
SKLTCECEHNTTGPDCGKCKKNYQGRPWSPGSYLPPIPKGTANTCIPSISSIGTNVCDNELH
CQNGGTCHNNVRCLCPAAYTGILCEKLRCEEAGSCGSDSGQGAPPHGTPALLLLTTLLGTAS
PLVF

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CCACGCGCTCCGGGTGAACCTGGGCCGAGCCCTCCCGCTCGGCTAAGATTGCTGAGGAGCGGC
CGGGTAGCTGGCAGGCGCCGACTTCCGAAGCGCCGCTCCGGGCGAGGTGTCCTCATGACTT
CTCTTGTGGACCATGTCCGTGATCTTTTTGCCTGCGTGGTACGGTAAGGGATGGACTGCC
CCTCTCAGCCTCTACTGATTTTTACCACACCCAAAGATTTTTTGAATGGAGGAGACGGCTCA
AGAGTTTAGCCTTGCGACTGGCCAGTATCCAGGTGAGGTTCTGCAGAAGGTTGTGACTTT
AGTATACATTTTTCTTCTTTCGGGGACGTGGCCTGCATGGCTATCTGCTCCTGCCAGTGTC
AGCAGCCATGGCCTTCTGCTTCTCGGAGACCCTGTGGTGGGAATTACAGACTTCTATGACA
CTACCTGCATTGGCCTAGCCTCCAGGCCATACGCTTTTCTTGAGTTTGACAGCATCATTCAG
AAAGTGAAGTGGCATTTTAACTATGTAAGTTCCTCTCAGATGGAGTGAGCTTGGAAAAAAT
TCAGGAGGAGCTCAAGTTGCAGCCTCCAGCGGTTCTACTCTGGAGGACACAGATGTGGCAA
ATGGGGTGATGAATGGTCACACCCGATGCACCTTGAGCGCTGCTCCTAATTTCCGAATGGAA
CCAGTGACAGCCCTGGGTATCTTCTCCTCATTTCTAACATCATGTGTGCTGCCCTGAATCT
CATTCGAGGAGTTTACCTTGCAGAACATTTTACAGGATCCAAGGAGCTGGTTCTGCTGGT
TGGACCAAACTCTGTGAGCCAGCCACCCCTGACCCAAATGAGGAGAGCTCTGATTCTCCCAT
CGGGGAGCAGTGATGTCAAACCTTCTGCTGCTGGGGAATCTCATCAGCAGGGAGCCTGTGGA
AAAGGGCATGTCAGTGAATCTGGGAATGGCTGGATTCGGAACATCTGCCATGTGTATTG
ATGGCAGAGCTGTTGCCACAAGCGCCTTTTATTAGGGTAAATTAACAAATCCATTCTAT
TCCTCTGACCCATGCTTAGTACATATGACCTTTAACCTTACATTTATATGATTCTGGGGT
GCTTCAGAAGTGTTATTTTCATGAATCATTCATATGATTGATCCCCAGGATCTATTTTGT
TTAATGGGCTTTTCTACTAAAAGCATAAAATAGCTGAGGCTGATTAGTCAGGGCAAAACCAT
TTACTTTACATATTCGTTTTCAATACTTGCTGCTCATGTTACAGCAAGCTTCTTACGGTTTTT
TTGTAACAATAAATATTTTGAGTAAATAAGGGTACATTTTAACAAACTCAGTAGTACAACC
TAAACTTGATATAAAGTGTTGTAATAAGTATAGCCATTTATATCCTATGTATAAATTAATG
AAGTGGCTTCAGAAATGGCAGAATAAATCTAAAGTGTTTATTAATAAAAAAAAAAAAAAAAAA
AAAAG

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FIGURE 76

MSVIFFACVVRDGLPLSASTDFYHTQDFLEWRRRLKSLALRLAQYPGRGSAEGCDFS IHF
SSFQDVACMAICSCQCPAAMAFCFLETLWWEFTASYDTTCIGLASRPYAFLEFDSIIQKVW
HFNYVSSQMECSLEKIQEELKLQPPAVLTLEDTDVANGVMNGHTPMHLEPAPNFRMEPVTA
LGILSLILNIMCAALNLIRGVHLAEHSLQDPRSWFCWLDQTS

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TOTTT-040660

FIGURE 77

TGCTTCCTGGAGACCCCTGTGGTGGGAATTCACAGCTTCNTATGACACTACCTGCATTGGCNT
AGCCTCCAGGCCATACGCTTTTCTTGAGTTTGACAGCATCATTCAGAAAAGTGAAGTGGCATT
TTAACTATGTAAGTTCCTNTCAGATGGAGTGCAGCTTGGAAAAAATTCAGGAGGAGCTCAAG
TTGCAGCCTCCAGCGGTTCTCANTATGGAGGACACAGATGTGGCAAATGGGGT

FIGURE 78

CTCAGCGGCGCTTCTCGTAGCGAGCCTAGTGGCGGGTGTTCGATTGAAACGTGAGCGCGA
 CCCGACCTTAAAGAGTGGGGAGCAAAGGAGGACAGAGCCCTTTAAACGAGGCGGGTGGTG
 CTTGCCCTTTAAGGGCGGGGCGTCCGGACGACTGTATCTGAGCCCCAGACTGCCCGAGTT
 TCTGTGCGAGGCTGCGAGGAAAGGCCCTAGGCTGGGTCTGGGTGCTTGGCGGCGGGCGCTT
 CCTCCCCGCTCGTCTCCCCGGGCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTA
TGGAAGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGC
GAGTGATTATATCAACACTTCTGTTTGAACACTGTACATCCTCTGCCACATCTTCTTGAC
CCGCTTCAAGAAGCCTGCTGAGTTACCACAGTGGATGATGAAGATGCCACCGTCAACAAGA
TTGCGCTCGAGCTGTGCACCTTTACCTGGCAATTGCCCTGGGTGCTGTCCTGCTCCTGCC
TTCTCCATCATCAGCAATGAGGTGCTGCTCTCCTGCTCGGAACACTACATCCAGTGGCT
CAACGGCTCCTCATCCATGGCCTCTGGAACCTTGTTTTCTCTTCCCCAACCTGTCCCTCA
TCTTCTCATGCCCCTTGCATATTTCTTCACTGAGCTGAGGGCTTTGCTGGCTCCAGAAAG
GGTGCTCTGGGCGGGTCTATGAGACAGTGGTGATGTTGATGCTCCTCACTCTGCTGGTGCT
AGGTATGGTGTGGGTGGCATCAGCCATTGTGGACAAGAACAAGGCCAACAGAGAGTCACTCT
ATGACTTTTGGGAGTACTATCTCCCCACCTTACTCATGCATCTCCTTCTTGGGGTCTG
CTGCTCCTGGTGTGTACTCCACTGGGTCTCGCCCGCATGTTCTCCGTCACTGGGAAGCTGCT
AGTCAAGCCCCGGCTGCTGGAAGACCTGGAGGAGCAGCTGTAAGTCTCAGCCTTTGAGGAGG
CAGCCCTGACCCGAGGATCTGTAATCCTACTTCTGCTGGCTGCCTTTAGACATGGAGCTG
CTACACAGACAGGTCTGGCTCTGACAGACAGAGGGTCTGCTGGAGAAGAGGCGGAAGCG
TTCAGCCTGGCAACGGAACCTGGGCTACCCCTGGCTATGCTGTGCTTGTGGTGTGACGG
GCCTGTCTGTGCTCATTGTGGCCATCCACATCCTGGAGCTGCTCATCGATGAGGCTGCCATG
CCCCAGGCATGCAGGGTACCTCCTTAGGCCAGGTCTCCTTCTCCAAGCTGGGCTCCTTTGG
TGCCGTCAATTCAGTTGTACTCATCTTTTACCTAATGGTGTCTCTCAAGTTGTGGGCTTCTATA
GCTCTCCACTCTTCCGGAGCCTGCGGCCAGATGGCAGCAGACTGCCATGACGCAGATAATT
GGGAACCTGTGCTCTCTCCTGGTCTTAAGCTCAGCACTTCTGTCTTCTCTCGAACCTGGG
GCTCACTCGCTTTGACCTGCTGGGTGACTTTGGACGCTTCAACTGGCTGGGCAATTTCTACA
TTGTGTTCTCTACACGCGAGCCTTTGCAGGCCCTACCACACTCTGTCTGGTGAAGACCTTC
CTCAGCTGTGCGGCGAGAGCTGATCCGGGCCCTTGGGCTGGACAGACTGCCGCTGCCCGT
CTCCGGTTTCCCCCAGGCATCTAGGAAGACCCAGCACCAGTGACCTCCAGCTGGGGTGGGA
AGGAAAAAACTGGACACTGCCATCTGCTGCCTAGGCCCTGGAGGGAAGCCCAAGGCTACTTGG
ACCTCAGGACCTGGAATCTGAGAGGTTGGGTGGCAGAGGGGAGCAGGCCATCTGCACTATT
GCAATAATCTGAGCCAGAGTTTGGGACCAGGACCTCCTGCTTTCCATACTTAAGTGTGGCCT
CAGCATGGGGTAGGCTGGGTGACTGGGTCTAGCCCCGATCCCAATCTGTTTACACATCA
ATCTGCCTCACTGCTGTTCTGGGCCATCCCCATAGCCATGTTTACATGATTGTGATGCAAT
AGGTTGGGTTAGGGGAGGAAAGGACTGGGCCAGGGCAGGCTCGGGAGATAGATTGTCTCC
CTTGCTCTTGCCCCAGCAGAGCCTAAGCATGTGCTATCCTGGAGGGGCTTGGACCACTG
AAAGACCAAGGGATAGGAGGAGGAGGCTTCAGCCATCAGCAATAAAGTTGATCCCAGGGA
 AAAAA

FIGURE 79

MEAPDYEVLSVREQLFHERIRECIISTLLFATLYILCHIFLTRFKKPAEFTTVDDDEDATVNK
IALELCTFTLAIALGAVLLLLPFSIISNEVLLSLPRNYIIQWLNGSLIHGLWNLVFLFPNLSL
IFLMPFAYFFTESEGFAGSRKGVLRVYETVVMLMLLTLLVLGMVWVASAIVDKNKANRESL
YDFWEYYLPYLYSCISFLGVLLLLVCTPLGLARMFSVTGKLLVKPRLLEDLEEQLYCSAFEE
AALTRRICNPTSCWLPLDMELLHRQVLAIQTQRVLLKRRKASAWQRNLGYPLAMLCLLVLT
GLSVLIVAIHILELLIDEAMPRGMQGTSLGQVSFSKLGSFGAVIQVVLIFYLMVSSVVGIFY
SSPLFRSLRPRWHDAMTQIIIGNCVCLLVSSALPVFSRTLGLTRFDLLGDFGRFNWLGIFY
IVFLYNAAFAGLTTLCLVKTFATAVRAELIRAFGLDRLPLPVSGFPQASRKTQHQ

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FIGURE 80

GGCTGCCGAGGGAAGGCCCCCTTGGGTTGGTCTTGGTTGCTTGGCGGCGGCGGNTTCNTCCCC
GCTCGTCCTCCCCGGGCCCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGAAGC
ACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCGAGTGTA
TTATATCAACACTTCTGTTTGCAACACTGTACATCCTCTGCCACATCTTCCTGACCCGCTTC
AAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCG

FIGURE 81

GACCGACCTTAAGAGTGGGAGCAAAGGGAGGACAGAGCCTTTTAAACGAGGCGGTGGTGC
CTGCCCTTTAAGGGCGGGGCGTCCGGACGACTGTATCTGAGCCCCAGACTGCCCGAGTTTC
TGTCGCAGGCTGCGAGGAAAGGCCCTAGGCTGGGTCTGGTGCTTGGCGGCGGCGGCTTCCT
CCCCGTTGTCNTCCCCGGGCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGA
AGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCGAGT
GTATTATATCAACACTTCTGTTTGCAACACTGTACATCNTCTGCCACATCTTCCTGACCCGC
TTCAAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCGTCAACAAGATTGC
GCTCGAGCTGTGCACCTTTACCTGGCAATTGCCCTGGGTGCTGTCTGCTCCTGCCCTTCT
CCATCATCAGCAATGAGGTGCTGCACTCCC

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FIGURE 82

GATGTGCTCCTTGGAGCTGGTGTGCAGTGTCCIGACTGTAAGATCAAGTCCAAACCTGTTTT
GGAATTGAGGAACTTCTCTTTTGATCTCAGCCCTTGGTGGTCCAGGTCTTCAATGCTGCTGT
GGGTGATATTACTGGTCCTGGCTCCTGTGAGTGGACAGTTTGCAAGGACACCCAGGCCCAT
ATTTTCCTCCAGCCTCCATGGACCACAGTCTTCCAAGGAGAGAGAGTGACCCTCACTTGCAA
GGGATTTTCGCTTCTACTCACCACAGAAAACAAAATGGTACCATCGGTACCTTGGGAAAGAAA
TACTAAGAGAAACCCAGACAATATCCTTGAGGTTTCAGGAATCTGGAGAGTACAGATGCCAG
GCCCAGGGCTCCCTCTCAGTAGCCCTGTGCACCTTGGATTTTTCTTCAGAGATGGGATTTCC
TCATGCTGCCCAGGCTAATGTTGAACTCCTGGGCTCAAGTGATCTGCTCACCTAGGCCTCTC
AAAGCGCTGGGATTACAGCTTCGCTGATCCTGCAAGCTCCACTTTCTGTGTTTGAAGGAGAC
TCTGTGGTTCTGAGGTGCCGGGCAAAGGCGGAAGTAACACTGAATAATACTATTTACAAGAA
TGATAATGTCTGGCATTCTTAATAAAAGAACTGACTTCCAAAAAAAAAAAAAAAAAAAAAA
AAA

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FIGURE 83

MLLWVILLVLAPVSGQFARTPRPIIFLQPPWTTVFQGERVTLTCKGFRFYSPQRTKWHRYL
GKEILRETPDNILEVQESGEYRCQAQGSPLSSPVHLDFSSEMGFPHAAQANVELLGSSDLLT

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FIGURE 84

CAGAGAGAGGGGGCTAGCTAGCTGTCTCTGCGGACCAGGGAGACCCCCGCGCCCCCGGTGTG
GAGGCGGCTTACAGGGCCGGGTGGGCTGGCGAGCCGACGCGGCGGCGGAGGAGGCTGTGAG
GAGTGTGTGGAACAGGACCCGGGACAGAGGAACCATGGTCTCGCAGAACCTGAGCACCTTTT
GCCTGTTGCTGCTATACCTCATCGGGCGGTGATTGCCGGACGAGATTTCTATAAGATCTTG
GGGTGCGCTCGAAGTGCTCTATAAAGGATATTAAGGCGCTATAGGAACTAGCCCTGCA
GCTTCATCCCGACCGGAACCTGATGATCCACAAGCCAGGAGAAATTCAGGATCTGGGTG
CTGCTTATGAGGTTCTGTGAGATAGTGAGAAACGGAACAGTACGATACTTATGGTGAAGAA
GGATTAAGATGGTCATCAGAGCTCCCATGGAGACATTTTTTACACTTCTTTGGGGATTT
TGTTTTCATGTTTGGAGGAACCCCTCGTCAGCAAGACAGAAATATCCAAGAGGAAGTGATA
TTATTGTAGATCTAGAAGTCACTTTGGAAGAAGTATATGCAGGAAATTTGTGGAAGTAGT
AGAAACAAACCTGTGGCAAGCGAGGCTCTGGCAACCGGAAGTGCAATGTCCGCAAGAGAT
CGGCAACCCAGCTGGGCGCTTGGGCGCTTCCAAATGACCCAGGAGGTGGTCTGCGACGAAT
GCCCTAATGTCAAAGTGTGATGAAGAAGCAAGCTGGGAAGTAGAAATAGAGCCTGGGGTG
AGAGACGGCATGGAGTACCCCTTTATTGGAGAAGGTGAGCCTCACGTGGATGGGAGCCTGG
AGATTACGGTTCGAATCAAAGTTGTCAAGCACCAATATTTGAAAGGAGAGGAGATGATT
TGTACACAAATGTGACAACTCTCATTAGTTGAGTCACTGGTTGGCTTTGAGATGGATATTACT
CACTTGGATGGTCACAAGGTACATATTTCCCGGGATAAGATCACCAGGCCAGGAGCGAAGCT
ATGGAAGAAAGGGGAAGGGCTCCCCAACTTTGACAACAACATATCAAGGGCTCTTTGATAA
TCACTTTTGATGTGGATTTTCCAAAAGAACGTTAACAGAGGAAGCGAGAGAAGGTATCAAA
CAGCTACTGAAACAAGGGTCAGTGCAAGAAGGTATACAATGGACTGCAAGGATATTGAGAGTG
AATAAAATTTGACTTTGTTTAAATAAGTGAATAAGCGATATTTATTATCTGCAAGGTTTTT
TTGTGTGTGTTTTTGTTTTTATTTTCAATATGCAAGTTAGGCTTAATTTTTTTATCTAATGA
TCATCATGAAATGAATAAGAGGGCTTAAGAAATTTGTCCATTGTGATTGCGAAAAGATGACC
AGCAAAAGGTTTACTAATACCTCTCCCTTTGGGGATTTAATGTCTGGTGTGCCCGCTGAGT
TTCAGAAATTAAGCTGCAAGAGGACTCCAGGAGCAAAAGAAACACAATATAGAGGGTTGGA
GTGTTTGTAGCAATTCATTCAAAATGCCAACTGGAGAAGTCTGTTTTTAAATACATTTTGTG
TTTATTTT

FIGURE 85

MAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRASIKDIKKAYRKLALQLHPDRNPDDPQ
AQEKFQDLGAAYEVLSDSEKRRQYDITYGEEGLKDGHQSSHGDI FSHFFGDFGFMFGGT PRQQ
DRNI PRGSDII VDLVLTLEEVYAGNFVEVVRNKPVARQAPGKRKCNCRQEMRTTQLGPGRFQ
MTQEVVCDECPNVKLVNEERTLEVEIEPGVRDGMETPFIFEGEPHVDGEPGDLRFRIKVVKH
PIFERRGDDLYTNVTISLVESLVGFEMDITHLDGHKVHISRDKITRPGAKLWKKGEGLPNFD
NNNIKGSIIITFDVDFPKEQLTEEAREGIKQLLKQGSVQKVYNGLQGY

Important features:**Signal peptide:**

amino acids 1-22

Cell attachment sequence.

amino acids 254-257

Nt-dnaJ domain signature.

amino acids 67-87

Homologous region to Nt-dnaJ domain proteins.

amino acids 26-58

N-glycosylation site.

amino acids 5-9, 261-265

Tyrosine kinase phosphorylation site.

amino acids 253-260

N-myristoylation site.

amino acids 18-24, 31-37, 93-99, 215-221

Amidation site.

amino acids 164-168

FIGURE 86

TGGGACCAGGGAACCCCGGGCCCCCGGTGGAGNGCCTAACAGGCCGGTGGNTGCGACCGAA
GCGGCGGGCGGAGGAGGTTTTTGAGGATTTTGGAAACAGGACCCGGACAGAGGAACCATGGTT
CCGCAGAACNTGAGCACNTTTTGCCGTGTTGNTGNTATACTTCATCGGGGCGGTGATTGCCGG
ACGAGATTTNTATAAGATTTTGGGGTGCCTNGAAGTGCCTTNTATAAAGGATATTAAGG
CCTATAGGAAACTAGCCCTGCAGNTTATCCCGACCGGAACCCCTGATGATCCACAAGCCCAG
GAGAAATTCAGGATTTGGGTGCTGCTTATGAGGTTNTGTCAGATAGTGAGAAACGGAACA
GTACGATAATTATGGTGAAGAAGGATTAAGATGGTNATCAGAGCTCCCATGGAGACATTT
TTTCACACTTNTTTGGGGATTTTGGTTTCATGTTTGGAGGAACCCCTNGTCAGCAAGACAGA
AATATTCCAAGAG

CCTATAGGAAACTAGCCCTGCAGNTTATCCCGACCGGAACCCCTGATGATCCACAAGCCCAG

FIGURE 87

GGCACGAGGCGGGCGGGGAGTCGCGGGATGCGCCCGGAGCCACAGCCTGAGGCCCTCAGGT
 CTCTGCAGGTGTCTGTGAGGAACCTAGCACCTGCCATCCTCTTCCCAATTTGCCACTTCCA
 GCAGCTTTAGCCCATGAGGAGGATGTGACCGGGACTGAGTCAGGAGCCCTCTGGAAGC**ATGG**
 AGACTGTGGTGATTGTTGCCATAGGTGTGCTGGCCACCATTCTTTGCGTTCGTTTGCAGCC
 TTGGTGCTGGTTTTGCAGGCAGCGCTACTGCCGCCGCGAGACCTGCTGCAGCGCTATGATTC
 TAAGCCCATTTGTGGACCTCATTGGTGCCATGGAGACCCAGTCTGAGCCCTCTGAGTTAGAAC
 TGGACGATGTCGTTATCACCAACCCCCACATTGAGGCCATTCTGGAGAATGAAGACTGGATC
 GAAGATGCCCTCGGGTCTCATGTCCCACTGCATTGCCATCTTGAAGATTTGTCACACTCTGAC
 AGAGAAGCTTGTGGCCATGACAATGGGCTCTGGGGCCAAGATGAAGACTTCAGCCAGTGTCA
 GCGACATCATTGTGGTGGCCAAGCGGATCAGCCCCAGGGTGGATGATGTTGTGAAGTCGATG
 TACCCTCCGTTGGACCCCAAACCTCCTGGACGCACGGACGACTGCCCTGCTCCTGTCTGTGACG
 TCACCTGGTGCTGGTGACAAGGAATGCCTGCCATCTGACGGGAGGCCCTGGACTGGATTGACC
 AGTCTCTGTGGCTGCTGAGGAGCATTGGAAGTCCTTCGAGAAGCAGCCCTAGCTTCTGAG
 CCAGATAAAGGCCCTCCAGGCCCTGAAGGCTTCTGCAGGAGCAGTCTGCAATT**TAGT**GGCCT
 ACAGGCCAGCAGCTAGCCATGAAGGCCCTGCCGCCATCCCTGGATGGCTCAGCTTAGCCTT
 CTACTTTTCTATAGAGTTAGTTGTTCTCCACGGCTGGAGAGTTCAGCTGTGTGTCATAG
 TAAAGCAGGAGATCCCCGTAGTTTATGCCTCTTTGCAGTTGCAAACTGTGGCTGGTGAGT
 GGCAGTCTAATACTACAGTTAGGGGAGATGCCATTCACTCTCTGCAAGAGGAGTATTGAAAA
 CTGGTGGACTGTCAGCTTTATTTAGCTCACCTAGTGTTTTCAAGAAAATTGAGCCACCGTCT
 AAGAAATCAAGAGGTTTCACATTAAATTAGAATTTCTGGCCTCTCTCGATCGGTGAGAATG
 TGTGGCAATTCTGATCTGCATTTTCAGAAGAGGACAATCAATTGAACTAAGTAGGGGTTTC
 TTCTTTTGGCAAGACTTGTA

METVIVIVAIGVLATIFLASFAALVLVCRQRYCRPRDLLQRYDSKPIVDLIGAMETQSEPSSEL
 ELDDVVITNPHIEAILENEDWIEDASGLMSHCIAILKICHTLTLEKLVAMTMGSGAKMKTSAS
 VSDIIVAKRISPRVDVVKSMYPPLDPKLLDARTALLSVSHLVLVTRNACHLTGGLDWI
 DQSLSAEEHLEVLREAALASEPKGLPGEGFLQEQSAI

GCTTCATTCTTCCGACTCAGCTTCCACCCTGGGCTTTCGAGGTGCTTTCGCCGTGTC
CCACCACCTGCAGCCATGATCTCCTTAAACGGACACGCAGAAAATTGGAATGGGATTAACAGGA
TTTGGAGTGTTTTCTGTCTTTTGAATGATTCTCTTTTTTGACAAAGCACTACTGGCTAT
TGAAATGTTTTATTGTAGCCGGCTTGGCTTTTGTAATTGGTTTAGAAAGAACATTAGAT
TCTTCTTCCAAAAACATAAAATGAAAGCTACAGGTTTTTTCTGGGTGGTGTATTGTAGTC
CTTATTGGTTGGCCTTTGATAGGCATGATCTTCGAAATTTATGGATTTTTCTCTGTTCAG
GGGCTTCTTCTGTCTGTTGTGGCTTTATTAGAAGAGTGCCAGTCCTTGATCCCTCCTAAAT
TTACCTGGAATTAGATCATTTGTAGATAAAGTTGGAGAAAGCAACAATATGGTATTAACAACA
AGTGAAATTTGAAGACTCATTTAAATATTGTGTTATTATAAAAGTCATTGAAGAATATTCA
GCACAAAATTAAATTACATGAAATAGCTTGTAAATGTTCTTTACAGGAGTTTAAAACGTATAG
CCTACAAAGTACCAGCAGCAAATTAGCAAAGAAGCAGTGAAAACAGGCTTCTACTCAAGTGA
ACTAAGAAGAAGTCAGCAAGCAAACCTGAGAGAGGTGAAATCCATGTTAATGATGCTTAAGAA
ACTCTTGAAGGCTATTGTGTGTTTTTCCACAATGTGCGAAACTCAGCCATCCTTAGAGAA
CTGTGGTGCTGTTTCTTTCTTTTATTTTGAAGGCTCAGGAGCATCCATAGGCATTGTGCT
TTTTAGAAGTGTCACATGCAATGGCAAAAATATTTCAGTTGCACTGTATCTCTGGAAGTGA
TGCATGAATTCGATTGGATTGTGTCATTTTAAAGTATTAAACCAAGGAACCCCAATTTTG
ATGTATGGATTACTTTTTTTTTGNGCNCAGGGCC

FIGURE 90

MISLTDTQKIGMGLTGFGVFFLFFGMILFFDKALLAIGNVLEFVAGLAFVIGLERTFRFFFQK
HKMKATGFFLGGVFVVLIGWPLIGMIFEIYGFFLLFRGFFPVVVGFIIRVPVLGSLNLNPGI
RSFVDKVGESNNMV

Important features:

Transmembrane domains:

amino acids 12-30 (typeII), 33-52, 69-89 and 93-109

N-myristoylation sites.

amino acids 11-16, 51-56 and 116-121

Aminoacyl-transfer RNA synthetases class-II protein.

amino acids 49-59

90/330-116-121

FIGURE 91

GAAGACGTGGCGGCTCTCGCCTGGGCTGTTTCCCGGCTTCATTTCTCCGACTCAGCTTCCC
ACCNTGGGCTTTCCGAGGTGCTTTCGCCGCTGTCCCACCACTGCAGCCATGATCTCCTTAA
CGGACACGCAGAAAATTGGAATGGGATTAACCGGATTGGAGTGTTTTTCCTGTTCTTTGGA
ATGATTCTCTTTTTTGACAAAGCACTACTGGCTATTGGAAATGTTTTATTTGTAGCCGGCTT
GGCTTTTGTAATTGGTTTAGAAAGAACATTCAGATTCTTCTTCCAAAACATAAAATGAAAG
CTACAGGTTTTTTCTGGGTGGTGTATTTGTAGTCCTTATTGGTTGGCCTTTGATAGGCATG
ATCTTCGAAATTTATGGATTTTTTCTCTTGTTT

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FIGURE 92

GGCACGAGGCTGAACCCAGCCGGCTCCATCTCAGCTTCTGGTTTCTAAGTCCATGTGCCAAA
GGCTGCCAGGAAGGAGACGCCCTTCTGAGTCCTGGATCTTTCTTCTCTGGAATCTTTGA
CTGTGGGTAGTTATTTATTTCTGAATAAGAGCGTCCACGCATC**ATG**GACCTCGCGGGACTGC
TGAAGTCTCAGTTCTCTGTGCCACCTGGTCTTCTGCTACGTCTTTATTGCCTCAGGGCTAATC
ATCAACACCATTTCAGCTCTTCACTCTCCTCCTCTGGCCCATTAACAAGCAGCTCTTCCGGAA
GATCAACTGCAGACTGTCTATTGCATCTCAAGCCAGCTGGTGATGCTGCTGGAGTGGTGGT
CGGGCACGGAATGCACCATCTTCACGGACCCGCGCCTACCTCAAGTATGGGAAGGAAAAAT
GCCATCGTGGTTCTCAACCACAAGTTTGAAATTGACTTTCTGTGTGGCTGGAGCCTGTCCGA
ACGCTTTGGGCTGTTAGGGGGCTCCAAGTCTTGCCCAAGAAAGAGCTGGCCTATGTCCCAA
TTATCGGCTGGATGTGGTACTTCACCGAGATGGTCTTCTGTTCGCGCAAGTGGGAGCAGGAT
CGCAAGACGGTTGCCACCAAGTTTGCAGCACCTCCGGGACTACCCCGAGAAGTATTTTTTCTCT
GATTTACTGTGAGGGCACACGGTTCACGGAGAAGAAGCATGAGATCAGCATGCAGGTGGCCC
GGGCCAAGGGGCTGCCTCGCCTCAAGCATCACCTGTTGCCACGAACCAAGGGCTTCGCCATC
ACCGTGAGGAGCTTGAGAAATGTAGTTTCAGCTGTATATGACTGTACACTCAATTTCAGAAA
TAATGAAATCCAACACTGCTGGGAGTCTAAACGGAAGAAATACCATGCAGATTTGTATG
TTAGGAGGATCCCACTGGAAGACATCCCTGAAGACGATGACGAGTGCTCGCCCTGGCTGCAC
AAGCTCTACCAGGAGAAGGATGCCTTTCAGGAGGAGTACTACAGGACGGGCACCTTCCGAGA
GACGCCCATGGTGCCCCCGCGGCCCTGGACCCTCGTGAACCTGGCTGTTTTGGGCCTCGC
TGGTGCTTACCCCTTTCTTCCAGTTCTGTGTCAGCATGATCAGGAGCGGTCTTCCCTGACG
CTGGCCAGCTTCATCTCGTCTTCTTTGTGGCCTCCGTGGGAGTTCGATGGATGATTGGTGT
GACGGAATTGACAAGGGCTCTGCCTACGGCAACTCTGACAGCAAGCAGAACTGAATGAC**T**
CACTCAGGGAGGTGTACCATCCGAAGGGAACCTTGGGGAACCTGGTGGCTCTGCATATCTT
CCTTAGTGGGACACGGTGACAAAGGCTGGGTGAGCCCTGCTGGGCACGGCGGAAGTCACGA
CCTCTCCAGCCAGGAGTCTGGTCTCAAGGCCGATGGGGAGGAAGATGTTTTGTAATCTTT
TTTTCCCATGTGCTTTAGTGGGCTTTGGTTTTCTTTTGTGCGAGTGTGTGTGAGAATGGC
TGTTGTGTGAGTGTGAACTTTGTCTGTGATCATAGAAAGGTATTTTAGGCTGCAGGGAG
GGCAGGGCTGGGGACCGAAGGGGACAAGTTCCCTTTTCATCCTTTGGTGTGAGTTTTCTGT
AACCCTTGGTTGCCAGAGATAAAGTGAAGTGCCTTTAGGTGAGATGACTAAATTATGCCTC
CAAGAAAAAAAATTAAGTGCTTTTCTGGGTCAAAAAAAAAA

FIGURE 93

MDLAGLLKSQFLCHLVFCYVFIASGLIINTIQLFTLLWPINKQLFRKINCRLSYCISSQLV
MLLEWWSGTECTIFTDPRAYLKYGKENAIVVLNHKFEIDFLCGWSLSERFGLGGSKVLAKK
ELAYVPIIGMMWYFTEMVFCSRKWEQDRKTVATSLQHLRDYPEKYFFLIHCEGTRFTEKKHE
ISMQVARAKGLPRLKHHLLPRTKGFATVRSRNVVSAVYDCTLNFRNNENPTLLGVLNGKK
YHADLYVRRIPLEDIPEDDDCSAWLHKLYQEKDAFQEYYRTGTFPETPMVPPRRPWTLVN
WLFWASLVLYPFFQFLVSMIRSGSSLTLASFILVFFVASVGVRWMIGVTEIDKGSAYGNSDS
KQKLND

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FIGURE 94

CTGAGGCGGCGGTAGC**ATG**GAGGGGGAGAGTACGTCGGCGGTGCTCTCGGGCTTTGTGCTCG
 GCGCACTCGCTTTCCAGCACCTCAACACGGACTCGGACACGGAAGGTTTTCTTCTTGGGAA
 GTAAAAGGTGAAGCCAAGAACAGCATTACTGATCCCAATGGATGATGTTGAAGTTGTTTA
 TACAATTGACATTGAGAAATATATTCCATGCTATCAGCTTTTTAGCTTTTATAATTCTTCAG
 GCGAAGTAAATGAGCAAGCACTGAAGAAAATATTATCAAATGTCAAAAAGAATGTGGTAGGT
 TGGTACAAAATCCGTCGTCATTGAGATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACAA
 AAACCTGTCAGGAGCATTTTTCAAACCAAGACCTTGTTTTCTGCTATTAAACCAAGTATAA
 TAACAGAAAGCTGCTCTACTCATCGACTGGAACATTCTTATATAAACCTCAAAAAGGACTT
 TTTACAGGGTACCTTTAGTGGTTGCCAATCTGGGCATGCTGAACAACTGGGTTATAAAAC
 TGTATCAGGTTCTGTATGTCCACTGGTTTTAGCCGAGCAGTACAAACACACAGCTCTAAAT
 TTTTTGAAGAAGATGGATCCTTAAAGGAGGTACATAAGATAAATGAAATGTATGCTTCATTA
 CAAGAGGAATTAAAGAGTATATGCAAAAAAGTGGAGACAGTGAACAAGCAGTAGATAAACT
 AGTAAAGGATGTAAACAGATTAAACGAGAAATTGAGAAAAGGAGAGGAGCACAGATTCAGG
 CAGCAAGAGAGAGAAGACATCCAAAAAGACCTCAGGAGAACATTTTTCTTTGTGTCAGGCATTA
 CGGACCTTTTTTCCAAATTTCTGAATTTCTTCATTCATGTGTTATGCTTTAAAAATAGACA
 TGTTCATAAAGTAGCTGTAACACCAACCACCTCGATGTAGTAGACAATCTGACCTTAA
 TGGTAGAACACACTGACATTCTGGAAGCTAGTCCAGCTAGTACACCACAAATCATTAAAGCAT
 AAAGCCTTAGACTTAGATGACAGATGGCAATTCAGAGATCTCGGTTGTTAGATACACAAGA
 CAAACGATCTAAAGCAAATACTGGTAGTAGTAACCAAGATAAAGCATCCAAATGAGCAGCC
 CAGAAACAGATGAAGAAATTGAAAAGATGAAGGGTTTTGGTGAATATTCACGGTCTCCTACA
 TTT**TGA**TCCCTTTTAAACCTTACAAGGAGATTTTTTTATTGGCTGATGGGTAAAGCCAAACAT
 TTCTATTGTTTTTACTATGTTGAGCTACTTGCAAGTAAAGTTTCTTTTACTATGTTTAC
 CTGTTTGCAAGTAATACAGATAACTCTTAGTGCAATTTACTTCACAAAGTACTTTTTCAAAC
 ATCAGATGCTTTTATTTCCAAACCTTTTTTTTACCTTTCTACTAAGTTGTTGAGGGGAAGGCT
 TACACAGACACATTTCTTAGAATTGGAAGTGAAGACAGGCACAGTGGCTCACACCTGTAA
 TCCCAGCACTTAGGGAAGACAAGTCAGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCC
 TGGGCAACGATTTAGAGCATTGCTATTAAAAATAAAATGGAAGCAAGAATAGCCTTAT
 TTTCAAAATATGGAAGAAATTTATATGAAAATTTATCTGAGTCATTAATTTCTCCTTAAG
 TGATACTTTTTTAGAAGTACATTATGGCTAGAGTTGCCAGATAAAATGCTGGATATCATGCA
 ATAAATTTGCAAAACATCATCTAAAATTTAAAAAAAAAAAAAAAAAAAAA

FIGURE 95

MEGESTSAVLSGFVLGALAFQHLNTDSDTEGFLLGVEVKGEAKNSITDSQMDDVEVVYTIIDQ
KYIPCYQLFSFYNSSGEVNEQALKKILSNVKKNVVGWYKFRRHSDQIMTFRRERLLHKNLQEH
FSNQDLVFLLLTPSIITESCSTHRLHSPLYKPKGLFHRVPLVVANLGMSEQLGKTVSGSC
MSTGFSRAVQTHSSKFFEEEDGSLKEVHKINEMYASLQEELKSICKKVEDSEQAVDKLVKDVN
RLKREIEKRGAQIQAAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKNRHVSKSS
CNYNHHLDVVDNLTLMEHTDIPEASPASTPQIIKHKALDLDRAWQFKRSRLDQTQDKRSKA
NTGSSNQDKASKMSSPETDEEIEKMKGFGEYSRSPTE

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[illegible]

FIGURE 97

MARFGLPALLCTLAVLSAALLAAELKSKSCSEVRRLYVSKGFNKNDAPLHEINGDHLKICPQ
GSTCCSQEMEKEYSLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKSLNDMF
VKTYGHLVMQNSSELFKDLFVELKRYVVGNNLEEMLNDFWARLLERMFRLVNSQYHFTDEY
LECVSKYTEQLKPFQDVPRKLKLVTRAFVAARTFAQGLAVAGDVVSKVSVVNPTAQCTHAL
LKMIYCSHCRGLVTVKPCYNYCSNIMRGCLANQGDLDFEWNNFIDAMLMVAERLEGPFNIES
VMDPIDVKISDAIMNQDNSVQVSQKVFQCGGPPKPLPAGRISRSISESAFSARFRPHHPEE
RPTTAAGTSLDRLVTDVKEKQAKKFWSSLPNSVCNDERMAAGNGNEDDCWNGKGKSRYLE
AVTGNGLANQGNNPEVQVDTSKPDILILRQIMALRVMTSKMKNAYNGNDVDFDISDESSGE
GSGSGCEYQQCPSEFDYNATDHAGKSANEKADSAGVRPGAQAYLLTVFCILFLVMQREWR

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CTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACAGGCTGAGTATCCT
GACCTGAGTCATCCCCAGGGATCAGGAGCCTCCAGCAGGGAACCTTCCATTATATTCTTCAA
GCAACTTACAGCTGCACCGACAGTTGCGAATGAAAGTTCTAATCTCTTCCCTCCTCTGTTGC
TGCCACTAATGCTGATGTCATGGTCTCTAGCAGCCTGAATCCAGGGGTGCGCAGAGGCCAC
AGGGACCGAGGCCAGGCTTCTAGGAGATGGCTCCAGGAAGGCGCCAGAATGTGAGTGCAA
AGATTGGTTCCTGAGAGCCCCGAGAAGAAAATTATGACAGTGTCTGGGCTGCCAAAGAAGC
AGTGCCCCCTGTGATCATTTCAGGGCAATGTGAAGAAAAAAGACACCAAAGGCACCACAGA
AAGCCAAACAAGCATTCCAGAGCCTGCCAGCAATTTCTCAAACAATGTGAGCTAAGAAGCTT
TGCTCTGCCTTTCTAGGAGCTCTGAGCGCCCACTCTTCCAATTAAACATTCTCAGCCAAGAA
GACAGTGAGCACACCTACCAGACACTTCTTCTCTCCACCTCACTCTCCCACTGTACCACC
CCTAAATCATTCCAGTGCTCTCAA¹AAAGCATGTTTTTCAAGATCATTTTGGTTGTTGCTCT
TCTAGTGCTCTTCTCTCTCGTCACTCTAGCCTGTGCCCTCCCCCTATCCGTTCTTAGGCTC
AATTACCTGAAAGATTCCAGGAACCTGTAGCTTCTTAGCTAGTGTCA²TTTAACTTAAATGC
AATCAGGAAAGTAGCAACAGAACTCAATAAATATTTTTAAATGTCAAAAAAAAAAAAAAAAAA

FIGURE 99

MKVLISLLLLLLPLMLMSMVSSSLNPGVARGHRDRGQASRRWLQEGGQECECKDWFLRAPRR
KFMTVSGLPKKQCPCDHFKGNVKKTRHQRHHRKPNKHSRACQQFLKQCQLRSFALPL

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FIGURE 100

AATGGCTGTCTTAGTACTTCGCCTGACAGTTGTCTCTGGGACTGCTTGTCTTATTCCTGACCT
GCTATGCAGACGACAAACCAGACAAGCCAGACGACAAGCCAGACGACTCGGGCAAAGACCCA
AAGCCAGACTTCCCAAAATTCCTAAGCCTCCTGGGCACAGAGATCATTGAGAATGCAGTCGA
GTTTCATCTCCGCTCCATGTCCAGGAGCACAGGATTTATGGAATTTGATGATAATGAAGGAA
AACATTTCATCAAAGTGAACATCCTCAGGACACACCCATGTGGCTCCTGGACAATCCAAGAGCA
GCCAAATCCTGCTTTTCCAGTTTGGCTCCACAAGTCCTCCAGGACAGAGCCCTCAAAGCAAC
TCCCAACGAGTTCTCAGGATTCAGGCTCTGGCTTCAACCAAACAGAACTCATTTTGAACACC
CTGACTGCATTTTGGCTTTTAGAAAGTTAGAATAAATATGGCGCTTTGGGATCACATAGTTG
ATGGAGAGGAAA

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FIGURE 101

MAVLVLRLTVVLGLLVFLTCYADDKPKPDDKPDGSGKDPKPDFPKFLSLLGTEIIENAVE
FILRSMRSTGFMFDDNEGKHSSK

104TTT*04406660

GGACGCCAGCGCCTGCAGAGGCTGAGCAGGGA~~AAAA~~AGCCAGTGCCCCAGCGGAAGCACAGCT
CAGAGCTGGTCTGCC~~ATG~~GACATCCTGGTCCCCTCTGCGAGCTGCTGGTGTCTTCTTAC
CCTGCCCTGCACCTCATGGCTCTGCTGGGCTGCTGGCAGCCCCCTGTGCA~~AAA~~AGCTACTTCC
CCTACCTGATGGCCGTGCTGACTCCCAAGAGCAACCGCAAGATGGAGAGCAAGAAACGGGAG
CTCTTCAGCCAGATAAAGGGGCTTACAGGAGCCTCCGGGAAAGTGGCCCTACTGGAGCTGGG
CTGCGGAACCGGAGCCAACCTTTCAGTTCTACCCACCGGGCTGCAGGGTCACTGCCTAGACC
CAAATCCCACCTTTGAGAAGTTCCTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATAT
GAGCGGTTTGTGGTGGCTCCTGGAGAGGACATGAGACAGCTGGCTGATGGTCCATGGATGT
GGTGGTCTGCACTCTGGTGTCTGTCTCTGTGCAGAGCCAAGGAAGTCTCTGCAGGAGGTCC
GGAGAGTACTGAGACCGGGAGGTGTCTCTTTTCTGGGAGCATGTGGCAGAACCATATGGA
AGCTGGGCCTTCTATGTGGCAGCAAGTTTTCGAGCCACCTGGA~~AA~~CACATTGGGGATGGCTG
CTGCCTCACCAGAGAGACCTGGAAGGATCTTGAGAACGCCAGTCTCCGAAATCCAATGG
AACGACAGCCCCCTCCCTTGAAGTGGCTACCTGTTGGGCCCCACATCATGGGAAAGGCTGTC
AAACAATCTTTCCAAGCTCCAAGGCACTCATTTGCTCCTCCCCAGCCTCCAATTAGAACA
AGCCACCCACCAGCCTATCTATCTTCCACTGAGAGGGACCT~~TAG~~CAGAATGAGAGAAGACATT
CATGTACCACCTACTAGTCCCTCTCTCCCCAACCTCTGCCAGGGCAATCTCTAACTTCAAT
CCGCCTTCGACAGTGA~~AAA~~AGCTCTACTTCTACGCTGACCCAGGGAGGAACACTAGGACCC
TGTTGTATCCTCAACTGCAAGTTTCTGGACTAGTCTCCAACGTTTGCTCTCCAATGTTGTCT
CCTTTCCTTCGTTCCCATGGTAAAGCTCCTCTCGCTTTCCTCCTGAGGCTACACCCATCGCT
CTCTAGGAAGTGGTCACAAAAGTCATGGTGCCTGCATCCCTGCCAAGCCCCCTGACCCTCT
CTCCCCACTACCACCTTCTTCTGAGCTGGGGGCACCAAGGGAATCAGAGATGCTGGGGAT
GCCAGCAAGCAAGCTCAAAGAGGCAGAGGTTTGTCTCAAATATTTTAAATAAATAGACGA
AACCAGC

FIGURE 103

MDILVPLLQLLVLLLTLPPLHLMALLGCWQPLCKSYFPYLMAVLTPKSNRKMESKKRELFSQI
KGLTGASGKVALLELGCCTGANFQFYPPGCRVTCLDPNPHEKFLTKSMAENRHLQYERFVV
APGEDMRQLADGSMDVVVCTLVLCVQSPRKVLQEVRRLRPGGVLFWEHVAEPIGSWAFM
WQQVFEPWTKHIGDGCCLTRETWKDLENAQFSEIQMERQPPPLKWLPGPHIMGKAVKQSFP
SSKALICSFPSLQLEQATHQPIYLPRLGT

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FIGURE 104

GTGGGATTTATTTGAGTGCAAGATCGTTTTCTCAGTGGTGGTGGAAAGTTGCCTCATCGCAGG
 CAGATGTTGGGGCTTTGTCCGAACAGCTCCCCCTCTGCCAGCTTCTGTAGATAAGGGTTAAAA
 ACTAATATTTATATGACAGAAGAAAAAGGATGTCAATTCGTAAGTAAACATCATCATCTTGG
 TCCTGGCTGTTGCTCTCTTCTTACTGGTTTTTGACCATAACTTCCTCAGCTTGAGCAGTTTG
 TTAAGGAATGAGGTTACAGATTACAGGAATTGTAGGGCCTCAACCTATAGACTTTGTCCAAA
 TGCTCTCCGACATGCAGTAGATGGGAGACAAGAGGAGATTCTGTGGTCATCGCTGCATCTG
 AAGACAGGCTTGGGGGGGCCATTGCAGCTATAAACAGCATTACAGCACAACACTCGCTCCAAT
 GTGATTTTCTACATTGTTACTCTCAACAATACAGCAGACCATCTCCGGTCTGGCTCAACAG
 TGATTCCCTGAAAAGCATCAGATACAAAATTGTCAATTTTGACCCTAACTTTTGGAAGGAA
 AAGTAAAGGAGGATCCTGACCAGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTTCTAC
 TTGCCAATTTCTGGTTCACAGCGCAAAGAAGGCCATATACATGGATGATGATGTAATTGTGCA
 AGGTGATATTCTTGCCCTTTACAATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAG
 AAGATTGTGATTCAGCCTCTACTAAAGTTGTATCCGTGGAGCAGGAAACCAGTACAATTAC
 ATTGGCTATCTTGACTATAAAAGGAAAGAAATTCGTAAGCTTTCCATGAAAGCCAGCACTTG
 CTCATTTAATCCTGGAGTTTTTGTGTGCAACCTGACGGAATGGAACGCAGAAATATAACTA
 ACCAACTGGA AAAATGGATGAAACTCAATGTAGAAGAGGGACTGTATAGCAGAACCCTGGCT
 GGTAGCATCACACACCTCCTCTGCTTATCGTATTTTATCAACAGCACTCTACCATCGATCC
 TATGTGGAATGTCGCCACCTTGTTCCAGTGCTGGAACGATATTCACCTCAGTTTGTA
 AGGCTGCCAAGTTACTCCATTGGAATGGACATTGGAAGCCATGGGGAAGGACTGCTTCATAT
 ACTGATGTTTGGGAAAAATGGTATATTCAGACCCAACAGGCAAAATTC AACCTAATCCGAAG
 ATATACCGAGATCTCAAACATAAAGTGAACAGAAATTTGAACTGTAAGCAAGCATTCTCAG
 GAAGTCTGGAAGATAGCATGCATGGGAAGTAACAGTTGCTAGGCTTCAATGCCTATCGGTA
 GCAAGCCATGGA AAAAGATGTGTGAGCTAGGTAAAGATGACAACTGCCCTGTCTGGCAGTC
 AGCTCCCGAGACAGACTATAGACTATAAATATGTCTCCATCTGCCTTACCAAGTGTCTTCTT
 ACTACAATGTGTAATGACTGGAAGAAGAACTGATATGGCTAGTTACAGTACGCTGGTACAGA
 TAATTC AAAACTGCTGTTGGTTTTAATTTGTAACTGTGGCTGATCTGTAATAAAACTT
 ACATTTTTT

FIGURE 105

MSFRKVNIIILVLAVALFLLVLHNFSLSSLLRNEVTDSGIVGFQPIDFVPNALRHAVDGR
QEEIPVVIAASEDRLGGAIAAINSIQHNTSRNVIFYIVTLNNTADHLRSWLNSDSLKSIRYK
IVNFDPKLLEGKVKEDPDQGESMKPLTFARFYLPILVPSAKKAIYMDDDVIVQGDILALYNT
ALKPGHAAAFSEDCDSASTKVVIRGAGNQYNYIGYLDYKKERIRKLSMKASTCSFNPGVFVA
NLTEWKRQNITNQLEKWMKLNVEEGLYSRTLGSITTPLLIVFYQQHSTIDPMWNVRHLGS
SAGKRYSPQFVKAAKLLHWNGHLKPWGRTASYTDVWEKWYIPDPTGKFNLIRRYTEISNIK

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FIGURE 106

TGGTTTTTGCCCCATAAATTCCTCAGCTTGAGCAGTTTGTTAAGGAATGAGGTTACAGATT
CAGGAATTNTAGGNCCTCAACCTNTAGANTTTGTCCCAAATGTTCTCCGACATGCAGTAGAT
GGGAGACAAGAGGAGATTCCCTGTGGTCATCGCTGCATNTGAAGACAGGCTTGGGGGGGCCAT
TGCAGCTATAAACAGCATTCAGCACAACTCGNTCCAATGTGATTTTCTACATTGTTACTC
TCAACAATACAGCAGACCATNTCCGGTCCTGGNTCAACAGTGATTCCCTGAAAAGCATCAGA
TACAAAATTGTCAATTTTGACCCTAACTTTTGAAGGAAAAGTAAAGGAGGATCCTGACCA
GGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTTCTACTTGCCAATTCTGGTTCCCAGCG
CAAAGAAGGCCATATACATGGATGATGATGTAATTGTGCAAGGTGATATTCTTGCCCTTTAC
AATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTCAGCCTCTAC
TAAAGTTGTCATCCGTGGAGCAGGAAA

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FIGURE 107

CGACGCTCTAGCGGTTACCGCTGCGGGCTGGCTGGGCGTAGTGGGGCTGCGCGGCTGCCACG
 GAGCTAGAGGGCAAGTGTGCTCGGCCAGCGTGCAGGGAACGCGGGCGGCAGACAACGGGC
 TGGGCTCCGGGGCCTGCGGCGCGGGCGCTGAGCTGGCAGGGCGGGTCGGGGCGCGGGCTGCA
 TCCGCATCTCCTCCATCGCCTGCAGTAAGGGCGGCCGCGCGAGCCTTTGAGGGGAACGACT
 GTGCGGAGCCCTAACAGGGGTGTCTCTGAGCCTGGTGGGATCCCCGAGCGTCACATCACT
 TTCCGATCACTTCAAAGTGGTTAAAACTAATATTTATATGACAGAAGAAAAAGATGTCATT
 CCGTAAAGTAAACATCATCATCTTGGTCTGGGCTGTGCTCTCTTCTTACTGTTTTGCAC
 CATAACTTCCTCAGCTTGAGGCAGTTTGTTAAGGAATGAGGTTACAGATTGAGGAATTGTAG
 GGCCTCAACCTATAGGACTTTGTCCCAAATGCTCTCCGACATGCAGTAGATGGGAGACAAGA
 GGAGATTCTGTGGTCATCGCTGCATCTGAAGACAGGCTTGGGGGGGCCATTGCAGCTATAA
 ACAGCATTCAGCACAACTCGCTCCAATGTGATTTTCTACATTGTTACTCTCAACAATACA
 GCAGACCATCTCCGCTCTGGGCTCAACAGTGATTCCCTGAAAAGCATCAGATACAAAATTG
 TCAATTTTGACCCTAAACTTTTGAAGGAAAAGTAAAGGAGGATCCTGACCAGGGGGAATCC
 ATGAAACCTTTAACTTTTGCAAGGTTCTACTTGCCAATTCTGGGTTCCGAGCGCAAGAAG
 CCATATACATGGATGATGATGTAATTGTGCAAGGTGATATTCTTGCCCTTTACAATACAGCA
 CTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTGAGCCTCTACTAAAGTTGT
 CATCCGTGGAGCAGGAACCCAGTACAATTACATTGGCTATCTTGACTATAAAAAGGAAAGAA
 TTCGTAAGCTTTCCATGAAAGCCAGCACTTGCTCATTTAATCCTGGAGTTTTTGTGCAAAC
 CTGACGGAATGGAACGACAGAATATAACTAACCACTGGAAAAATGGATGAACTCAATGT
 AGAAGAGGGACTGTATAGCAGAACCCTGGCTGGTAGCATCACAACACCTCCTCTGCTTATCG
 TATTTTATCAACAGCACTCTACCATCGATCCTATGTGGAATGTCCGCCACCTTGGTCCAGT
 GCTGGAAAACGATATTACCTCAGTTTGTAAGGCTGCCAAGTTACTCCATTGGAATGGACA
 TTTGAAGCCATGGGGAAGGACTGCTTCATATACTGATGTTTGGGGAAAAATGGTATATTCCA
 GACCCAACAGGCAAAATTCACCTAATCCGAAGATATACCGAGATCTCAAACATAAAGTGAA
 CAGAATTTGAACTGTAAGCAAGCATTTCTCAGGAAGTCTGGAAGATAGCATGCGTGGGAAG
 TAACAGTTGCTAGGCTTCAATGCCTATCGGTAGCAAGCCATGGAAAAAGATGTGTGAGCTAG
 GTAAAGATGACAACTGCCTGTCTGGCAGTCAGCTTCCAGACAGACTATAGACTATAAAT
 ATGTCTCCATCTGCCTTACCAAGTGTCTTCTTACTACAAATGCTGAATGACTGGAAGAAGAA
 CTGATATGGCTAGTTCAGCTAGCTGGTACAGATAATTCAAACCTGCTGTTGGTTTTAATTTT
 GTAACCTGTGGCCTGATCTGTAAATAAACTTACATTTTTCAATAGGTAAGAAAAA
 AAAAAA

CGGCGGCTGCCACG
 GAGCTAGAGGGCAAGTGTGCTCGGCCAGCGTGCAGGGAACGCGGGCGGCAGACAACGGGC
 TGGGCTCCGGGGCCTGCGGCGCGGGCGCTGAGCTGGCAGGGCGGGTCGGGGCGCGGGCTGCA
 TCCGCATCTCCTCCATCGCCTGCAGTAAGGGCGGCCGCGCGAGCCTTTGAGGGGAACGACT
 GTGCGGAGCCCTAACAGGGGTGTCTCTGAGCCTGGTGGGATCCCCGAGCGTCACATCACT
 TTCCGATCACTTCAAAGTGGTTAAAACTAATATTTATATGACAGAAGAAAAAGATGTCATT
 CCGTAAAGTAAACATCATCATCTTGGTCTGGGCTGTGCTCTCTTCTTACTGTTTTGCAC
 CATAACTTCCTCAGCTTGAGGCAGTTTGTTAAGGAATGAGGTTACAGATTGAGGAATTGTAG
 GGCCTCAACCTATAGGACTTTGTCCCAAATGCTCTCCGACATGCAGTAGATGGGAGACAAGA
 GGAGATTCTGTGGTCATCGCTGCATCTGAAGACAGGCTTGGGGGGGCCATTGCAGCTATAA
 ACAGCATTCAGCACAACTCGCTCCAATGTGATTTTCTACATTGTTACTCTCAACAATACA
 GCAGACCATCTCCGCTCTGGGCTCAACAGTGATTCCCTGAAAAGCATCAGATACAAAATTG
 TCAATTTTGACCCTAAACTTTTGAAGGAAAAGTAAAGGAGGATCCTGACCAGGGGGAATCC
 ATGAAACCTTTAACTTTTGCAAGGTTCTACTTGCCAATTCTGGGTTCCGAGCGCAAGAAG
 CCATATACATGGATGATGATGTAATTGTGCAAGGTGATATTCTTGCCCTTTACAATACAGCA
 CTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTGAGCCTCTACTAAAGTTGT
 CATCCGTGGAGCAGGAACCCAGTACAATTACATTGGCTATCTTGACTATAAAAAGGAAAGAA
 TTCGTAAGCTTTCCATGAAAGCCAGCACTTGCTCATTTAATCCTGGAGTTTTTGTGCAAAC
 CTGACGGAATGGAACGACAGAATATAACTAACCACTGGAAAAATGGATGAACTCAATGT
 AGAAGAGGGACTGTATAGCAGAACCCTGGCTGGTAGCATCACAACACCTCCTCTGCTTATCG
 TATTTTATCAACAGCACTCTACCATCGATCCTATGTGGAATGTCCGCCACCTTGGTCCAGT
 GCTGGAAAACGATATTACCTCAGTTTGTAAGGCTGCCAAGTTACTCCATTGGAATGGACA
 TTTGAAGCCATGGGGAAGGACTGCTTCATATACTGATGTTTGGGGAAAAATGGTATATTCCA
 GACCCAACAGGCAAAATTCACCTAATCCGAAGATATACCGAGATCTCAAACATAAAGTGAA
 CAGAATTTGAACTGTAAGCAAGCATTTCTCAGGAAGTCTGGAAGATAGCATGCGTGGGAAG
 TAACAGTTGCTAGGCTTCAATGCCTATCGGTAGCAAGCCATGGAAAAAGATGTGTGAGCTAG
 GTAAAGATGACAACTGCCTGTCTGGCAGTCAGCTTCCAGACAGACTATAGACTATAAAT
 ATGTCTCCATCTGCCTTACCAAGTGTCTTCTTACTACAAATGCTGAATGACTGGAAGAAGAA
 CTGATATGGCTAGTTCAGCTAGCTGGTACAGATAATTCAAACCTGCTGTTGGTTTTAATTTT
 GTAACCTGTGGCCTGATCTGTAAATAAACTTACATTTTTCAATAGGTAAGAAAAA
 AAAAAA

FIGURE 108

CTGCAGGTAGACATCTCCACTGCCCAGGAATCACTGAGCGTGACAGACAGCACAGCCTCCTCT
 GAAGGCCCGCCATACCAGAGTCCTGCCTCGGCATGGGCCTCACCATTGAGGCAGCTCCACTG
 TCTGTGCTGGTCTGAGGGTGCTGCCTGTCA**ATG**GGGGCAGCCATCTCCCAGGGGGCCCTCATC
 GCCATCGTCTGCAACGGTCTCGTGGGCTTCTTGCTGCTGCTGCTCTGGGTCATCCTCTGCTG
 GGCTGCCATTCTCGTCTGCCGACGTTGACTCTCTCTCTGAATCCAGTCCCAACTCCAGCCC
 TGGCCCCCTGCTCTGAGAAGGCCCCACCACCCAGAACCCAGCCATGAAGGCAGCTACCTGC
 TGCAGCCCTGAAGGCCCTGGCCTAGCCTGGAGCCCAGGACCT**TAA**GTCCACCTCACCTAGAG
 CCTGGAATTAGGATCCCAGAGTTCAGCCAGCCTGGGGTCCAGAACTCAAGAGTCCGCCTGCT
 TGGAGCTGGACCCAGCGGCCAGAGTCTAGCCAGCTTGGCTCCAATAGGAGCTCAGTGGCCC
 TAAGGAGATGGGCCTGGGGTGGGGCTTATGAGTTGGTGCTAGAGCCAGGGCCATCTGGACT
 ATGCTCCATCCCAGGGCCAAGGGTCAGGGGCCGGGTCCACTCTTTCCCTAGGCTGAGCACC
 TCTAGGCCCTCTAGGTTGGGGAAGCAAACCTGGAACCCATGGCAATAATAGGAGGGTGTCAG
 GCTGGGCCCTCCCTGGTCTCCAGTGTTTGCTGGATAATAAATGGAACCTATGGCTCTAA
 AAAAAAAAAAAAAAAAAA

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 TTTT.1431

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FIGURE 109

MGA AISQGALIAIVCNGLVGFLLLLLWVILCWACHSRLPTLTLSLNPVPTPALAPVLRPHH
PRSPAMKAATCCSPEGWPWSLEPRT

00990440.11401
T04TTT*04406660

GTTTTGAATTCCCTTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCCAGGCTACCA
 GTTCTCTCAAAGCAAGTCATTTCCCTTATTTAACCGATGTGTCCCTCAAACACCTGAGTGCTA
 CTCCTTATTTGCATCTGTTTTGATAAATGATGTTGACACCCTCCACCGAATTCCTAAGTGGA
 TCATGTCGGGAAGAGATACAATCCTTGGCCTGTGTATCCTCGCATTAGCCCTGTCTTTGGCC
 ATGATGTTTACCTTCAGATTCATCACCACCTTCTGGTTCACATTTTCATTTTCATTGTTAT
 TTTGGGATGTGTTGTTGTCTGCGGTGTTTTATGGTGGCTGTATTATGACTATACCAACGACC
 TCAGCATAGAATTTGGACACAGAAAGGGAAAAATATGAAGTGCCTGCTGGGGTTTGCATCGTA
 TCCACAGGCATCACGGCAGTGCTGCTCGTCTTGATTTTTGTCTCAGAAAGAGAATAAAAT
 GACAGTTGAGCTTTTCCAAATCACAAATAAAGCCATCAGCAGTGCTCCCTTCCTGCTGTTCC
 AGCCACTGTGGACATTTGCCATCCTCATTTTCTCTGGGTGCTCTGGGTGGCTGTGCTGCTG
 AGCCTGGGAACCTCAGAGAGCTGCCAGGTTATGGAAGCGGCCAAGTGAATATAAGCCCTT
 TCTGGGCATTCGTCAGATCTGTGCTGCTACCATTTAAATGGCCCTCATCTGGACTAGTGAAATCA
 TCCTTGCCTGCCAGCAATGACTATAGCTGGGGCAGTGTTTACTTGTATTTCACACAGAAGT
 AAAAAATGATCCTCCTGATCATCCCATCCTTTCGTCTCTCTCCATTCTCTTCTTCTACCATCA
 AGGAACCGTTGTGAAAGGGTCATTTTTAATCTCTGTGGTGAGGATTCGAGAATCATTGTCA
 TGTACATGCAAAACGCACTGAAAGAACAGCAGCATGGTGCAATTGTCCAGGTACCTGTTCCGA
 TGCTGCTACTGCTGTTTCTGGTGTCTTGACAAATACCTGCTCCATCTCAACCAGAATGCATA
 TACTACAACCTGCTATTAATGGGACAGATTTCTGTACATCAGCAAAAGATGCATTCAAATCT
 TGTCCAAGAACTCAAGTCACTTTACATCTATTAAGTGTCTTGAGACTTCATAATTTTTCTA
 GGAAAGGTGTTAGTGGTGTGTTTCACTGTTTTTGGAGGACTCATGGCTTTTAACTACAATCG
 GGCATTCCAGGTGTGGGCAGTCCCTCTGTTATTGGTAGCTTTTTTGGCTACTTAGTAGCCC
 ATAGTTTTTTATCTGTGTTTGAACCTGTGCTGGATGCATTTTCCCTGTGTTTTGCTGTTGAT
 CTGGAACAAATGATGGATCGTCAGAAAAGCCCTACTTTATGGATCAAGAATTTCTGAGTTT
 CGTAAAAAGGAGCAACAAATTTAAACAATGCAAGGACAGCAGGACCAAGCACTCATTAAAGGA
 ATGAGGAGGGAACAGAACTCAGGCCATTGTGAGATAGATACCCATTTTAGGTATCTGTACCT
 GTAAAAACATTTCCCTCTAAGAGCCATTACAGAAATAGAAGATGAGACCACTAGAGAAAAGTT
 AGTGAATTTTTTTTTTAAAGACCTAATAAACCTATTCTCTCTCAAAA

FIGURE 111

MSGRDTILGLCILALALSLAMMFTFRFITLLVHIFISLVILGLLFVCGVLWWLYDYTNDL
SIELDTERENMKCVLGFAIVSTGITAVLLVLIFVLRKRIKLTVELFQITNKAISSAPFLLFQ
PLWTFAILIFFWVLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFI
LACQQMTIAGAVVTCYFNRSKNDPPDHPILSSLSILFFYHQGTVVKGSFLISVVRIPRIIVM
YMQNALKEQQHGALSRYLFRCCYCCFWCLDKYLLHLNQNAYTTTAINGTDFCTSAKDAFKIL
SKNSSHFTSINCFGDFIIFLGKVLVVCFTVFGGLMAFNYNRAQVWAVPLLLVAFFAYLVAH
SFLSVFETVLDALFLCFAVDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNARAQQDKHSLRN
EEGTELQAIVR

1000000.11100

FIGURE 112

GTTCGATTAGCTCCTCTGAGAAGAAGAGAAAAGTTCTTGGACCTCTCCCTGTTTCTTCTCCTT
 AGAATAATTTGTATGGGATTTGTGATGCAGGAAGCCCTAAGGGAAAAAGAATATTCATTCTG
 TGTGGTGAATAATTTTGGAAAAAAATTCCTTCTTCAAACAAGGGGTGCATTCTGATATT
TATGAGGACTGTTGTTCTTCATATGAAGGCATCTGTTATTGAAATGTTCTCTGTTTGTGCTGG
 TGACTGGAGTACATTCAAACAAGAAACGGCAAAGAGATTAAAGGCCCAAGTTCACTGTG
 CCTCAGATCAACTGCGATGTCAAAGCCGGAAGATCATCGATCCTGAGTTTCATTGTGAAATG
 TCCAGCAGGATGCCAAGACCCCAAATACCATGTTTATGGCACTGACGTGTATGCATCCTCAT
 CCAGTTGTGTGGCGCTGCCGTACACAGTGGTGTGCTTGATAATTTCAGGAGGGAAAAATACTT
 GTTCGGAAGGTTGCTGGACAGTCTGGTTACAAAGGGAGTTATTCACCGGTGTCCAATCGTT
 ATCCCTTACCACGATGGAGAGAATCCTTTATCGTCTTAGAAAGTAAACCCAAAAAGGGTGTA
 ATACCCCATCAGCTCTTACATACTCATCATCGAAAAGTCCAGCTGCCCAAGCAGGTGAGACC
 ACAAAGCCCTATCAGAGGCCACCTATTCAGGGACAACCTGCACAGCCGGTCACTCTGATGCA
 GCTTCTGGCTGTCACTGTAGCTGTGGCCACCCCAACCTTGCCAAGGCCATCCCTCTCTG
 CTGCTTCTACCAACAGCATCCCCAGACCACAACTCAGTGGGCCACAGGAGCCAGGAGATGGAT
 CTCTGGTCCACTGCCACCTACACAAGCAGCCAAACAGGCCCAGAGCTGATCCAGGTATCCA
 AAGGCAAGATCCTTCAGGAGCTGCCCTTCAGAAACCTGTTGGAGCGGATGTGACGCTGGGAC
 TTGTTCCAAAAGAAGAATTGAGCACACAGTCTTTGGAGCCAGTATCCCTGGGAGATCCAAAC
 TGCAAAATGACTTGTCTGTTTAAATGATGGGAGCACCAGCATTTGGCAACCGCGATTCGG
 AATCCAGAAGCAGCTCCTGGCTGATGTTGCCAAGCTCTTGACATTGGCCCTGCCGCTCCAC
 TGTATGGTGTGTGTCAGTATGGAGACAACCTGCTACTCACTTTAACTCAAGACACACAG
 AATTTCTCGATCTGAAGACAGCCATAGAGAAAATTACTCAGAGAGGAGGACTTTCTAATGT
 AGGTGGGCCATCTCCTTTGTGACCAAGAACTCTTTTCCAAAGCCAATGGAACAGGAAGCG
 GGCTCCCAATGTGGTGGTGGTGGATGGTGGATGGCTGGCCACGGACAAAGTGGAGGAGGCT
 TCAAGACTTGGCAGAGAGTCAGGAATCAACATTTTCTTCATCACCATTGAAGGTGCTGCTGA
 AATGAGAAGCAGTATGTGGTGGAGCCCACTTTGCAACAAGGCCGTGTGCAGAACAAACG
 GCTTCTACTCGCTCCAGCTGCAGAGCTGGTGTGGCCTCCACAAGACCTCGACGCTCTGGT
 AAGCGGGTCTGCAGACTGACCGCTGGCTGGCTGCAGCAAGACCTGCTTGAATCGGCTGACAT
 TGGCTTGGCTCATCGACGGCTCCAGCAGTGTGGGACGGGCAACTTCGCGACCGCTCCTCCAGT
 TTGTGACCAACCTCACCAGAGGTTTGAGATTTCCGACACGGACAGCGGCTCGGGGGCTG
 CAGTACACCTACGAACAGCGGCTGGAGTTTGGGTCGACAAGTACAGCAGCAAGCCTGACAT
 CCTCAACGCCATCAAGAGGGTGGGCTACTGGAGTGGTGGCACCAGCAGCGGGGCTGCCATCA
 ACTTTCGCCCTGGAGCAGCTCTTCAAGAAGTCCAAGGCCAACAGAGGAAGTTAATGATCCTC
 ATCACCAGCGGGAGGTCCTACGACGACGTCGGGATCCAGCCATCGCCTGCCATCTGAAGGG
 AGTGATCACTTACGAGATAGGCGTTGCCCTGGGCTGCCCAAGAGGAGCTAGAAGTATGTGCCA
 CTACCCCGCCAGAGACCACTCTTCTTTGTGGACGAGTTTGACAACCTCATCATGATGTG
 CCCAGGATCATCCAGAACATTTGTACAGAGTTCAACTCACAGCCTCGGAAC**TGA**ATTACAG
 CAGGCAGACACCAAGTGTGCTTACTAAGTACGTGTTGGACCAACCCACCGCTTAA
 TGGGGCAGCCAGCGTGCAATCAAGTCTTGGGCAGGGCATGGAGAAACAAATGCTCTTGTATTAT
 TTCTTTGCCATCAATGCTTTTTCATATTCAAAACCTTGGAGTTACAAAGATGATCAACAACGT
 ATAGAATGAGCCAAAGGCTACATCATGTTGAGGGTGTGAGAGATTTCATATTTGACAATT
 GTTCTTCAAATTAATGTTGCGAATACAGTGCAGCCCTACGACAGGCTTACGTAGAGCTTTT
 GTGAGATTTTAAAGTTGTTATTCTGATTTGAATCTGTAAACCTCAGCAAGTTTCAATTTTT
 GTCATGACAATTAGGAATGCTGAATTAATGTTTGAAGGATGAAAAATAAAAAA
 AA
 AAAG

FIGURE 113

MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINCVDKAGKIIDPEFIVKC
PAGCQDPKYHVGTDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYNSGVQSL
SLPRWRESFIVLESKPKKGVTPSALTYSSSKSPAAQAGETTKAYQRPPIPGTTAQPVTLMQ
LLAVTVAVATPTTLPRPSPSAASTTSIPRPQSVGHRSQEMDLWSTATYTSSQNRPRADPGIQ
RQDPSGAAFQKPVGADVSLGLVPKEELSTQSLEPVSLSGDPNCKIDLSFLIDGSTSIGKRRFR
IQKQLLADVAQALDIGPAGPLMGVVQYGDNPATHTNLTHTNSRDLKTAIEKITQRGGLSNV
GRAISFVTKNFFSKANGNRSGAPNVVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAAE
NEKQYVVEPNFANKAVCRTNGFYSLHVQSWFGLHKTLPVLRVCDTDRLACSKTCLNSADI
GFVIDGSSSVGTGNFRITVLQFVTNLTKEFEISDITRIGAVQYTYEQRLEFGFDKYSSKPDIL
LNAIKRVGYWGGTSTGAAINFALQLFKKSKPNKRKLMILITDGRSYDDVRIPAMAAHLKG
VITYAIGVAWAAQEELEVIATHPARDHSFFVDEFDNLHQYVPRIIQNICTEFNSQPRN

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FIGURE 114

CAGGATGAACTGGTTGCAGTGGCTGCTGCTGCTGCGGGGGCGCTGAGAGGACACGAGCTCTA
TCCCCTTTCCGGCTGCTCATCCCGCTCGGCCTCCTGTGCGCGCTGCTGCCTCAGCACCATGGT
 GCGCCAGGTCCCAGCGCTCCGCGCCAGATCCCGCCCACTACAGTTTTTCTCTGACTCTAAT
 TGATGCACTGGACACCTTGCTGATTTTGGGGAATGTCTCAGAATTCCAAAGAGTGGTTGAAG
 TGCTCCAGGACAGCGTGGACTTTGATATTGATGTGAACGCCTCTGTGTTGAAACAAACATT
 CGAGTGGTAGGAGGACTCCTGTCTGCTCATCTGCTCTCCAAGAAGGCTGGGGTGGAGTAGA
 GGCTGGATGGCCCTGTTCCGGGCCTCTCCTGAGAATGGCTGAGGAGCGGCCCCGAAACTCC
 TCCAGCCTTTCCAGACCCCACTGGCATGCCATATGGAACAGTGAACCTACTTCATGCGGTG
 AACCCAGGAGAGACCCCTGTACCTGTACGGCAGGGATTGGGACCTTCATTGTTGAATTTGC
 CACCCTGAGCAGCCTCACTGGTGACCCGGTGTTCGAAGATGTGGCCAGAGTGGCTTTGATGC
 GCCTCTGGGAGAGCCGGTCAGATATCGGGCTGGTCGGCAACCACATTGATGTGCTCACTGGC
 AAGTGGGTGGCCAGGACGCAGGCATCGGGGCTGGCGTGGACTCCTACTTTGAGTACTTGGT
 GAAAGGAGCCATCCTGCTTCAGGATAAGAAGCTCATGGCCATGTTCTTAGAGTATAACAAAG
 CCATCCGGAACACACCCGCTTCGATGACTGGTACCTGTGGGTTCAGATGTACAAGGGGACT
 GTGTCCATGCCAGTCTTCAGATCCTTGGAGGCCACTTGGCCTGGTCTTCAGAGCCTCATTTGG
 AGACATTGACAATGCCATGAGGACCTTCCTCAACTACTACACTGTATGGAAGCAGTTTGGGG
 GGCTCCCGGAATTCTACAACATTCCTCAGGGATACACAGTGGAGAAGCGAGAGGGCTACCCA
 CTTGGCCAGAACTTATTGAAAGCGCAATGTACCTCTACCGTGCCACGGGGGATCCACCCCT
 CCTAGAACTCGGAAGAGATGCTGTGGAATCCATTGAAAAAATCAGCAAGGTGGAGTGCAGAT
 TTGCAACAATCAAAGATCTGCGAGACCACAAGCTGGACAACCCGATGGAGTCGTCTTCTCTG
 GCCGAGACTGTGAAATACCTCTACCTCCTGTTTGACCCAACCAACTTCATCCACAACAATGG
 GTCCACCTTCGACGCGGTGATCACCCCTATGGGGAGTGCATCCTGGGGGTGGGGGGTACA
 TCTTCAACACAGAAGCTCACCCCATCGACCTTGCCGCCCTGCACTGCTGCCAGAGGCTGAAG
 GAAGAGCAGTGGGAGGTGGAGGACTTGATGAGGGAATCTACTCTCTCAAACGGAGCAGGTC
 GAAATTTTCAGAAAAACATGTTAGTTTCGGGGCCATGGGAACCTCCAGCAAGGCCAGGAACAC
 TCTTCTCACCAGAAAACCATGACCAGGCAAGGGAGAGGAAGCCTGCCAAACAGAAGGTCCCA
 CTTCTCAGCTGCCCCAGTCAGCCCTTCACCTCCAAGTTGGCATTACTGGGACAGGTTTTCTCT
 AGACTCCTCATAACCACTGGATAATTTTTTATTTTTATTTTTTTGAGGCTAAACTATAATA
 AATTGCTTTTGGCTATCATAAAA

FIGURE 115

MPFRLLIPLGLLCALLPQHHGAPGPDGSAPDPAHYSFSLTLIDALDTHLLILGNVSEFQRVVE
VLQDSVDFDIDVNASVFETNIRVVGGLLSAHLLSKKAGVEVEAGWPCSGPLLRMAEEEAARKL
LPAFQTPTGMPYGTVNLLHGVNPGETPVTCTAGIGTFIVEFATLSSLTGDVPVFEDVARVALM
RLWESRSDIGLVGNHIDVLTGKWVAQDAGIGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNK
AIRNYTRFDDWYLVWQMYKGTVSMVPVFQSLEAYWPGLSLIGDIDNAMRTFLNYYTVWKQFG
GLPEFYNIPOGYTVEKREGYPLRPELIESAMYLYRATGDPPTLLELGRDAVESIEKISKVECG
FATIKDLRDHKLDRMESFFLAETVKYLYLLFDPTNFIHNNGSTFDAVITPYGECILGAGGY
IFNTEAHPIDLAALHCCQRLKEEQWEVEDLMREFYSLKRSRSKFQKNTVSSGPWEPPARPGT
LFSPENHDQARERKPAKQKVPLLSCPSPFTSKLALLGQVFLDSS

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FIGURE 116

AAGGTACATTTTCTCTGGAACCTCTCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTG
 GGCAGAAAGGAGGGTGCTTCGGAGCCCGCCCTTTCTGAGCTTCTTGGCCCGCTCTAGAACAA
 ATTCAGGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTTCTGAAGAAAGATGGCT
 GAGATGGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGGTCAAACCTAGTCTACCA
 AATGCAGACTTTCCACAATGGTTCTAGAAGAAATCTGGACAAGTCTTTTCATGTGGTTTTTCT
 ACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGCCTGCCCTCAGAACCTC
 TCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCAGTGATCGCGCCTGGAGA
 AACAGTGTACTATTCTGTGGAATACCAAGGGGAGTACGAGAGCCTGTACACGAGCCACATCT
 GGATCCCCAGCAGCTGCTGCTCACTCACTGAAGGTCTGAGTGTGATGTCACTGATGACATC
 ACGGCCACTGTGCCATACAACCTTCGTGTCAAGGCCACATTGGGCTCACAGACCTCAGCCTG
 GAGCATCTCGAAGCATCCCTTTAATAGAAACTCAACCATCTTACCCGACCTGGGATGGAGA
 TCACCAAAGATGGCTTCACCTGGTTATTGAGCTGGAGGACCTGGGGCCAGTTTGAGTTC
 CTTGTGGCCTACTGGAGGAGGGAGCCTGGTGCCGAGGAACATGTCAAATGGTGAGGATGG
 GGGTATTCAGTGCACCTAGAAACATGGAGCAGCTGGGCTGCATAGTGTGAAGGCCAGAGA
 CATTCTGTGAAGGCCATTGGGAGTACAGCGCTTCAGGCCAGACAGAATGTGTGGAGGTGCAA
 GGAGAGGCCATTCCCTGGTATCTGCCCCTGTTTGCCCTTGTTGGCTTCATGCTGATCCTTGT
 GGTCTGTGCCACTGTTCTGCTGGAATAAGGCCGCTGCTCCAGTACTCCTGTTGCCCGTGG
 TGGTCTCTCCAGACACCTTGAAATAAACCAATTACCCAGAAAGTTAATCAGCTGCAGAAGG
 GAGGAGGTGGATGCTGTGCCACGGCTGTGATGTCTCCTGAGGAACCTCCTCAGGGCCTGGAT
 CTCATAGAGTTTGCAGGAGGGCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAACCC
 ATGAGGGGACAAGTTGTGTTTCTGTTTTCCGCCACGGACAAGGGATGAGAGAAGTAGGAAGA
 GCCTGTTGTCTACAAGTCTAGAAGCAACCATCAGAGGCAGGGTGGTTGTCTAACAGAACAC
 TGACTGAGGCTTAGGGATGTGACCTCTAGACTGGGGCTGCCACTTGCTGGCTGAGCAACC
 CTGGGAAAAGTGACTTCATCCCTTCGGTCCCTAAGTTTTCTCATCTGTAATGGGGGAATTACC
 TACACACCTGCTAAACACACACACAGAGTCTCTCTATATATACACAGTACACATAAA
 TACACCCAGCACTTGCAAGGCTAGAGGGAAACTGGTGACACTCTACAGTCTGACTGATTTCAG
 TGTTCCTGGAGAGCAGGACATAAATGTATGATGAGAATGATCAAGGACTCTACACACTGGGT
 GGCTTGGAGAGCCACTTTCCAGAAATAATCCTTGAGAGAAAAGGAATCATGGGAGCAATGG
 TGTGAGTTCACCTCAAGCCCAATGCCGGTGCAGAGGGGAATGGCTAGCAGCCTCTACAGT
 AGGTGACCTGGAGGAAGGTCACAGCCACACTGAAAATGGGATGTGCATGAAACAGCGGATC
 CATGAACTACTGTAAAGTGTTGACAGTGTGTGCACACTGCAGACAGGAGGTGAAATGTATGT
 GTGCAATGCGACGAGAATGCAGAAGTCAGTAACATGTGTGCATGTTTGTGTGCTCCTTTTTTC
 TGTTGGTAAAGTACAGAATTACGCAATAAAAAGGCCACCCTGGCCAAAAGCGGTAATAAAA
 AAAAAAAAAA

FIGURE 117

MQTFTMVLEEIWTSLFMWFFYALIPCLLTDEVAILPAPQNLSVLSTNMKHLMLMWSPIAPGE
TVYYSVEYQGEYESLYTSHIWI PSSWCSLTEGPECVTDITATVPYNLRVRATLGSQTS
SILKHFFNRRNSTILTRPGMEITKDGHLVIELEDLGPQFEFLVAYWRREPGAEEHVKMVRSG
GIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVQGEAIPVLALFAFVGFMILIV
VVPLFVWKMGRLLQYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATAVMSPEELLRAWIS

Important features:**Signal peptide:**

amino acids 1-29

Transmembrane domain:

amino acids 230-255

N-glycosylation sites.

amino acids 40-43 and 134-137

Tissue factor proteins homology.

amino acids 92-119

Integrins alpha chain protein homology.

amino acids 232-262

FIGURE 118

TCCTGCTGATGCACATCTGGGTTTGGCAAAAGGAGGTTGCTTCGAGCCGCCCTTTCTAGCTT
CCTGGCCGGCTCTAGAACAATTAGGCTTCGCTGCGACTAGACCTCAGCTCCAACATATGCA
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGG
TCAAACCTGAGTCTACCAAATGCAGACTTTCACAAATGGTTCTAGAAGAAATCTGGACAAGTCT
TTTCATGTGGTTTTTCTACGCATTGATTCCATGTTTGTCTACAGATGAAGTGGCCATTCTGC
CTGCCCTCAGAACTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCA
GTGATCGCGCCTGGAGAAACAGTGTACTATTCTGTCCAATACCAGGGGGAGTACGAGAGCCT
GTACACGAGCCACATCTGGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTG
ATGTCACCTGATGACATCACGGCCACTGTGCCATACAACCTTTGTGTCAAGGCCACATTGGGC
TCACAGACCTCAGCCTGGAGCATCTGAAGCATCCCTTAAATAGAAACTCAACCTACCTTAC
CCGACCTGGGATGGAGATCACCAGAAATGGCTTGNACCTGGTTAGCTTAGCTGAGGACCAAGG
GGCCCCAGTTTGAGTTCCTTCTGTGCCTANTGGAGAGGGCGAACCCCTTCGCGCGCAAGGG
GTTCGCGAACCCCTTCGCGCGCTGGGGTATCTCTCGAGAAAGAGAGGCCCAATATGACCCAC
ATATCAATATGACGAANTGCTATTGTCCACCTGTTTGAGTGGCGCTGGGTTGAT

FIGURE 119

CGGACGCGTGGGCCGCCACCTCCGGAACAAGCCATGTGGCGGCGACGGTGGCAGCGGCGTG
 GCTGCTCCTGTGGGCTGCGGCTGCGCGCAGCAGGACAGGACACTTCTACGACTTCAAGGCGG
 TCAACATCCGGGGCAAACCTGGTGTGCTGGAGAAGTACCGCGGATCGGTGTCCCTGGTGGTG
 AATGTGGCCAGCGAGTTCGGCTTACAGACCAGCACTACCGAGCCCTGCAGCAGCTGCAGCG
 AGACCTGGGCCCCCACCACCTTTAACGTGCTCGCCTTCCCCTGCAACCAGTTTGGCCAACAGG
 AGCCTGACAGCAACAAGGAGATTGAGAGCTTTGCCCGCCGACCTACAGTGTCTCATTCCCC
 ATGTTTAGCAAGATTGCAGTCACCGGTACTGGTGCCCATCCTGCCTTCAAGTACCTGGCCCA
 GACTTCTGGGAAGGAGCCACCTGGAACCTTCTGGAAGTACCTAGTAGCCCCAGATGGAAGG
 TGGTAGGGGCTTGGGACCCAACTGTGTCACTGGAGGAGGTGAGACCCAGATCACAGCGCTC
 GTGAGGAAGCTCATCCTACTGAAGCGAGAAGACTTATTAAACCACCGCGTCTCCTCCTCCACCA
 CCTCATCCGCCCCACCTGTGTGGGGCTGACCAATGCAAACCTCAAATGGTGTCTCAAAGGGAG
 AGACCCACTGACTCTCCTTCCCTTTACTCTTATGCCATTGGTCCCATCATTTCTGTGGGGGAA
 AAATTCTAGTATTTTGATTATTTGAATCTTACAGCAACAAATAGGAACCTCGGCCAATGAG
 AGCTCTTGACCAGTGAATCACCAGCCGATACGAACGCTTGTGCAACAAAAATGTGTGGCAAA
 TAGAAGTATATCAAGCAATAATCTCCACCCCAAGGCTTCTGTAACCTGGGACCAATGATTAC
 CTCATAGGGCTGTTGTGAGGATTAGGATGAAATACCTGTGAAAGTGCCTAGGCAGTGCCAGC
 CAAATAGGAGGCATTCAATGAACATTTTTTGCATATAAACCAAAAATAACTTGTTATCAAT
 AAAAAGTGCATCCAACATGAATTTCCAGCCGATGATAATCCAGGCCAAAGGTTTGTGTTGTT
 GTTATTTCTCTGTATTATTTTCTTCATTACAAAAGAAATGCAAGTTTCATTGTAACATCCA
 AACAAATACCTCACGATATAAAATAAAAAATGAAAGTATCCTCCTCAAAA

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FIGURE 120

MVAATVAAAWLLLWAAACAQQEQDFYDFKAVNIRGKLVSLVKYRGSVSLVVNVASECGFTDQ
HYRALQQQLQRDLGPHHFNVLAFFPCNQFGQQEPDSNKEIESFARRTYSVSFPMFSKIAVTGTG
AHPAFKYLAQTSGKEPTWNFWKYLVA PDGKVVGAWDPTVSVEEVRPQITALVRKLILLKREDL

0000000.11101

CGGACGCGTGGGCGGGCCGGGACGCAAGCGAGCCATGCGCTGTCTACGTCGGGATGCT
TGCGCCTGGGGAGGCTGTGCGCCGGGAGCTCGGGGGTGCTGGGGGCCCGGGCGGCCCTCTCT
CGGAGTTGGCAGGAAGCGAGTTGCAAGGTGTCGCGTTCTCTAGTCCAGAGAGGTGGATGCT
CATGGTCTCCACGCCCATCGGAGGCTCAGCTACGTTACAGGGTGCACCAAAAAGCATCTTA
ACAGCAAGAGCTGTGGGCGAGCTGCTGGAGACCCAGCAGCAGAGGGTCCCAGAACGAGAGGCC
TTGTCGTCTCTCATGAAGACGTCAAGTTGACCTTTGCCAACTCAAGAGGAGGTGGACAA
AGCTGCTTCTGGCCTCTGAGCATTTGGCTCTGCAAAGGTGACCGGCTGGGCATGTGGGGA
CTAACTCTATGCATGGGTGCTCATGCACTTGGCCACCGCCAGGCGGCTCATTTCTGT
TCTGTGAACCCAGCCTACAGGCTATGGAACTGAGTATGCTCTCAAGAAAGGTGGGCTGCAA
GGCCCTTGTGTTTCCCCAAGCACTTCAAGACCCAGCAATTAACAAGTCTCTGAAGCAGATCT
TCTCAGAAAGTGAGAAATGCCAGCAGGGGCTTGAAGATCAGAGGCTCCGAGATCTGACC
ACAGTCATCTCGGTGGATGCCCTTTTGGCGGGGACCTTGCTCCTGGATGAAGTGGTGGCGGC
TGGGACGACACCGGAGCATCTGGACAGGCTCCAATACCAACAGCAGTCTCTGCTCTGCATAT
ACCCCTACAACATTCAGTTCACTTCGGGGACACAGGAGGCCCAAAGGGGGCCACCTCTCC
CACTACAACATTTGTCAACAACCCAACATTTTAGGAGAGCGCTGAAACTGCATGAGAAGAC
ACCAAGCAGAGTTGGCGATGATCTCTGCCAACCCCTGTACCAATTGCTGTGGGTTCCGTGGCAG
GCACAATGATGTGCTGATGTACGTTGCGACCTCATCTGGGCTCTCCATCTTCAATGGC
AAGAAGGCATGAGAGGCATCAGCAGAGAGAGGACACCTTCTGTAATGGTACCCCAAGCA
GTTCGTGGACATCTGCAACACAGCCAGACTTCCAGGTTATGACATCTCGACATGTGTGGAG
GTGTCAATTGCTGGTCCCTGCACCTCCAGAGTTGATCCGAGCATCATCAACAAGATAAAT
ATGAAGGACCTGTGTTGCTTATGGAACAACAGAGAAGTCAGCTGATATCTCGGCATCT
CCCTGAGGACCTGTGAGCAGAAGGACAAAGCGTGAGCAGAAATATGCTCAACAGGAGG
CCCGGATCATGAACATGGAGGCAAGGACGCTGGCAAAGCTGAACACGCCCGGGGAGCTGTGC
ATCCGAGGATCTGCGCTATGCTGGGCTATCGGGTGAGCCTCAGAGACAGAGAAGAGAGT
GGATCAGGACAAGTGGTATTTGACAGGAGATGTGCCCAATGAATGAGCAGGGCTCTCTCA
AGATGTGGGCGCTTAAGGATATCTGATCTCGGGGTGGTGAGAACATCTACCCCGCAGAG
CTCGAGGACTCTTTTCAACACACAGGAGTGCAGAGTGCAGGAAGTGCAGGTGGTGGGAGTAGGA
CGATCGGATGGGGGAGAGATTTGTGCTGCATCTCGGCTGAGGACGGGAGGAGACACGG
TGGAGGAGATAAAAGCTTTCTGCAAAAGGAAGATCTCTCACTCAAGATTCGAGAGTACATC
GTGTTTGTCAAAATACCCCTCACCAATTTCAGAAAGATCCAGAAATCAAACTTCTGAGA
CGAGATGGAACGACATCTAAATCTGTGAATAAAGCAGAGGCTGTCTGGCCGGTTTGGCTT
GACTCTCTCGTGTGAGATGCAACTGGCTTTATGCACTAGATGTCCCAAGCACCAGTTT
TGAGCCAGGCATCAATTAAGCAATTAAGCACTGAGCAAGCACTAAGAGCTCTGGATGGGTCT
CGGGAACCTGCCTTGGGCACAAGGTGCCAAAAGGCAGGAGCTGTCCAGGCCCTCCCTCTGT
TCCATCCCCACATTTCCCGCTGCTGTCTGTGATTGGCATAAAGAGCTCTGTGTTTCTTT
GAAAAAAAAAAAAAA

MAVYVGMRLRLGRLCAGSSGVLGARAALSRSQEARLQGVRLSSREVD RMVSTPIGGLSVYQ
GCTKKHLN SKTVGQCLETTAQRVPEREALVVLHEDVRLTFAQLKEEVKAASGLLSIGLCKG
DRLGMWGPNSYAWVLMQLATAQAGIILVSVNPAYQAMEYVLKKVGCKALVFPKQFKTQQY
YNVLKQICPEVENAQPGALKSQRLPDLTTVISVDAPLPGLTLLDEVVAAGSTRQHLDQLQYN
QQFLSCHDPINIQFTSGTTGSPKGATLSHYNIVNNSNILGERLKLHEKTPEQLRMILPNPLY
HCLGSVAGTMCM MYGATLILASPIFNGKKALEAISRERGTFLYGTPTFMFDILNQPDFSSY
DISTMCGGVIAGSPAPPELIRAIINKINMKDLVVAYGTTENS PVTFAHFPEDTVQKAESVG
RIMPHTEARIMNMEAGTLAKLNTPGELCIRGYCVMLGYWGEPQKTEEAVDQDKWYWTGDVAT
MNEQGFCKIVGRSKDMIIRGENIYPAELEDDFFHTHPKVQEVQVGVKDDRMGEEICACIRL
KDGEETTVEEIKAFCKGKISHFKIPKYIVFTVNYPLTISGKIQKFKLREQMERHLNL

amino acids 1-22

amino acids 140-161, 213-229, 312-334

amino acids 260-271

amino acids 19-24, 22-27, 120-125, 203-208, 268-273, 272-277,
314-319, 318-323, 379-384, 380-385, 409-413

amino acids 282-285

FIGURE 123

CAACTCCAACATTTTAGGAGAGCGCCTGAAACTGCATGAGAAGACACCAGAGCAGTTGCGGA
TGATCCTGCCCAACCCCTGTACCATTCGCTGGGTTCCGTGGCAGGCACAATGATGTGTCTG
ATGTACGGTGCCACCCTCATCTGGCCTCTCCCATCTTCAATGGCAAGAAGGCACTGGAGGC
CATCAGCAGAGAGAGAGGCACCTTCTGTATGGTACCCCCACGATGTTTCGTGGACATTCTGA
ACCAGCCAGACTTCTCCAGTTATGACATCTCGACCATGTGTGGAGGTGTCATTGCTGGGTCC
CCTGCACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAATATGAAGGACCTGGTGGT
TGCTTATGGAACCACAGAGAACAGTCCCGTGACATTCGCGCACTTCCCTGAGGACACTGTGG
AGCAGAAGGCAGAAAGCGTGGGCAGAATTATGCCTCACACGGAGGCGCGGATCATGAACATG
GAGGCAGGGACGCTGGCAAAGCTGAACACGCCCCGGGGAGCTGTGCATCCGAGGGTACTGCGT
CATGCTGGGCTACTGGGGTGAGCCTCAGAAGACAGAGGAAGCAGTGGATCAGGACAAGTGGT
ATTGGACAGGAGATGTCGCCAC

123-040660

FIGURE 124

GAGCAGGACGGAGCCATGACCCCGCCAGGAAAGCAGGTGCCAGGCCATGATCTGGACTGC
 AGGCTGGCTGCTGCTGCTGCTTCCGCGAGGAGCGCAGGCCCTGGAGTGCTACAGCTGCG
 TGCAGAAAGCAGATGACGGATGCTCCCCGAACAAGATGAAGACAGTGAAGTGC GCGCGGGC
 GTGGAGCTCTGCACCGAGGCCGTGGGGCGGTGGAGACCATCCACGGACAATCTCGCTGGC
 AGTGCGGGGTGCGGTTCCGGACTCCCCGGCAAGAATGACCGCGGCTGGATCTTACGGGC
 TTCTGGCGTTTCATCCAGCTGCAGCAATGCGCTCAGGATCGTGCAACGCCAAGCTCAACCTC
 ACCTCGCGGGCGCTCGACCCGGCAGGTAATGAGAGTGCATACCCGCCAACGGCGTGGAGTG
 CTACAGCTGTGTGGGCTGAGCCGGGAGGCGTGCCAGGGTACATCGCGCGGCTCGTGAGCT
 GCTACAACGCCAGCGATCATGTCTACAAGGGTGCTTCGACGGCAACGTACCTTGACGGCA
 GCTAATGTGACTGTGTCTTGCTGTCCGGGGCTGTGTCCAGGATGAATCTGCACCTCGGGA
 TGGAGTAACAGGCCAGGGTTCACGCTCAGTGGCTCCTGTTGCCAGGGGTCCCGCTGTAAT
 CTGACCTCCGCAACAAGACCTACTTCTCCCTCGAATCCCAACCCCTTGTCGGCTGCCCCCT
 CCAGAGCCCACGACTGTGGCTCAACACATCTGTCAACACTTCTACCTCGGCCCCAGTGAG
 ACCACATCCACCACCAACCCATGCCAGCGCCAACAGTCAGACTCCGAGACAGGGAGTAG
 AACACGAGGCCTCCCGGGATGAGGAGCCAGGTTGACTGGAGGCGCGCTGGCCACCAGGAC
 CGCAGCAATTCAGGGCAGTATCCTGCAAAAGGGGGCCCCAGCAGCCCCATAATAAGGCTG
 TGTGGCTCCACAGCTGGATTGGCAGCCCTTCTGTTGGCCGTGGCTGCTGGTGTCTACTGT
GAGCTTCTCCACCTGGAAATTTCCCTCTCACCTACTTCTCTGGCCCTGGGTACCCCTCTTCT
 CATACTTCCTGTTCCCACCACTGGACTGGGCTGGCCAGCCCCTGTTTTTCCAACATTTCCC
 CAGTATCCCCAGCTTCTGCTGCGCTGGTTTGCGGCTTTGGGAAATAAAATACCGTTGTATAT
 ATTCTGCCAGGGGTGTTCTAGCTTTTTGAGGACAGCTCCTGTATCCTTCTCATCCTTGTCTC
 TCCGCTTGTCTCTTGTGATGTTAGGACAGAGTGAGAGAAGTCAGCTGTACGGGGAAGGTG
 AGAGAGAGGATGCTAAGCTTCTACTCACTTTCTCCTAGCCAGCTGGACTTTGGAGCGTGG
 GGTGGGTGGGACAATGGCTCCCCACTCTAAGCACTGCCTCCCCTACTCCCCGCATCTTTGGG
 GAATCGGTTCCCATATGTCTTCTTACTAGACTGTGAGCTCCTCGAGGGGGGGCCCGGTAC
 CCAATTGCGCCTATAGTGAGTCGTA

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FIGURE 125

MDPARKAGAQAMIWTAGWLLLLLLRGGAQALECYSCVQKADDGCSFNKMKTVKCAPGVDVCT
EAVGAVETIHGQFSLAVRGCGSLPGKNDRGLDLHGLLAFIQLQQCAQDRCNAKLNLSRAL
DPAGNESAYPPNGVECYSCVGLSREACQGTSPPVVSCYNASDHVYKGCDFGNVTLTAANVTV
SLPVRGCVQDEFCTRDGVTGPGFTLSGSCCQGSRCNSDLRNKTYFSPRIPLVRLPPPEPTT
VASTTSVTTSTSAFVRPTSTTKMPAPTSQTPRQGEHEASRDEEPRLTGGAAGHQDRSNG
QYPAKGGPQQPHNKGCVAPTAGLAALLLAVAAGVLL

104111-0440660

CGGGACTCGGCGGGTCTCTCTGGGAGTCTCGGAGGGGACCGGCTGTGCAGACGCC**ATG**GAGT
TGGTGTCTGGTCTTCTCTGCAGCCTGCTGGCCCCATGGTCTTGGCCAGTGCAGCTGAAAAG
GAGAAGGAAATGGACCCTTTTCATTATGATTACCAGACCCTGAGGATTGGGGACTGGTGTT
CGCTGTGGTCTCTTCTCGGTTGGGATCCTCCTTATCCTAAGTCGCAGGTGCAAGTGCAGTT
TCAATCAGAAGCCCCGGGCCCCAGGAGATGAGGAAGCCCAAGTGGAGAACCTCATCACCGCC
AATGCAACAGAGCCCCAGAAGCAGAGAAC**TGA**GTGCAGCCATCAGTGGAAAGCCTCTGGAA
CCTGAGGCGGCTGCTTGAACCTTTGGATGCAAAATGTCTGATGCT**TAA**GAAAACCGGCCACTTC
AGCAACAGCCCTTCCCCAGGAGAAGCCAAGAACTTGTGTGTCCCCACCCTATCCCCCTA
ACACCATTCTCCACCTGATGATGCAACTAACTTGCTCCCCACTGCAGCCTGCGGTCT
GCCACCTCCCGTGATGTGTGTGTGTGTGTGTGTGTGACTGTGTGTGT**TG**CTAACTGTG
GTCTTTGTGGCTACTTGT**TG**TGGATGGTATTGT**TTG**TAGTGA**ACT**TGGACTCGCTTT
CCCAGGCAGGGGCTGAGCCACATGGCCATCTGACCTCCCTCCCCCTGGCCCTCCATCAC
CTTCTGCTCTTAGGAGGCTGCTTGTGCCCGAGCAGCCCCCTCCCTGATTTAGGGA**TG**
TAGGGTAAAGAGCAGGGCAGTGGTCTTCA**GT**CGTCTTGGGACCTGGGAAGGTTTGCAGCAC
TTTGT**CAT**CA**TTCT**CATGGACTCCTTCACTCCTTTAA**CA**AAAACTTGTCTCCTATCCC
ACCTGATCCAGTCTGAAGGTCTCTTAGCAACTGGAGATACAAAGCAAGGAGCTGGTGA**GC**
CAGCGTTGACGTAGGCAGGCTATGCCCC**TCC**GTGGTTAA**TTCT**TCCAGGGGCTTCCAG
AGGAGTCCC**AT**CTGCCCCGCCCTT**CAC**AGAGCGCCCGGGGATTCCAGGCCAGGGCTCT
ACTCTGCCCTGGGGAA**TGT**GTCCCCTGCATATCTTCTAGCAATA**ACT**CCATGGGCTCTGG
GACCTACCCCTTCCAACCTTCCCTGCTTCTGAGACTTCAATCTACAGCCAGCTCATCCAG
ATGCAGACTACAGTCCCTGCAAT**TGG**GTCTCTGGCAGGCAATAGTTGAAGGACTCCTGT**TCC**
GTTGGGGCCAGCACACCGGGATGGATGGAGGGAGAGCAGAGGCCTTTGCTTCTTGCCTACG
TCCCCTTAGATGGGCAGCAGAGGCAACTCCCGCATCCTTTGCTCTGCCTGT**CG**TGGT**CAG**
GCGGTGAGCGAGGTGGGTTGGAGACTCAGCAGGCTCCGTGCAGCCCTTGGGAACAGTGA**GC**
GTTGAAGGTCATAACGAGAGTGGGA**ACT**CA**ACC**AGATCCCGGCTCCCTGTCTCTGT**TT**
CCCGCGAAACCAACCA**ACCT**GC**GT**GC**GT**GACCAATTGCTTCTCTGATCTCTGATCTAT
CCTCAACAACAACAGAAAAAGGAATAAATATCCTTTGTCTCT

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FIGURE 127

MELVLVFLCSLLAPMVLASAAEKEKEMDPFHYDYQTLRIGGLVFAVVLFSVGILLILSRCK
CSFNQKPRAPGDEEAQVENLITANATEPQKQRTFVQPSGGLWNLRRLLLEPLDANVDA

0990440.11401

FIGURE 128

AAACTTGACGCC**ATGA**AAGATCCCGGTCCTTCCTGCCGTGGTGCTCCTCTCCCTCCTGGTGCT
CCACTCTGCCAGGGAGCCACCCTGGGTGGTCCTGAGGAAGAAAGCACCATTTGAGAATTATG
CGTCACGACCCGAGGCCTTTAACACCCCGTTTCCTGAACATCGACAAATTGCGATCTGCGTTT
AAGGCTGATGAGTTCCTGAACTGGCACGCCCTCTTTGAGTCTATCAAAGGAAACTTCCTTT
CCTCAACTGGGATGCCTTTCCTAAGCTGAAAGGACTGAGGAGCGCAACTCCTGATGCCCAGT**T**
GACCATGACCTCCACTGGAAGAGGGGGCTAGCGTGAGCGCTGATTCTCAACCTACCATAACT
CTTTCCTGCCTCAGGAACTCCAATAAACATTTCCATCCAAA

00990100-11490

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FIGURE 129

MKIPVLPAVVLSSLVLHSAQGATLGGPEEESTIENYASRPEAFNTPFLNIDKLRSFAKADE
FLNWHALFESIKRKL PFLNWD A FPKLGLRSATPDAQ

090049.11401
TCHTT"040660

FIGURE 130

CAGTTCTGAAATCAATGGAGTTAATTTAGGGAATACAAACCAGCCATGGGGGTGGAGATTGC
CTTTGCCTCAGTGATTCTCACCTGCCTCTCCCTTCTGGCAGCAGGAGTCTCCAGGTTGTTT
TTCTCCAGCCAGTTCCAACCTCAGGAGACAGGTCCCAAGGCCATGGGAGATCTCTCCTGTGGC
TTTGCCGGCCACTCATGAGAGTGTTTTTGTGTAAAGTATTTTTAGAATACTGTTGACTTCT
TCATGATTTAATAACCATCCTTIGCGAAGTTTTATGAGGCTTTAGGGGAATGTCAACCCCTCA
AATTTTTGTTATACTAGATGGCTTCATTTACCACCACTATTTTAAGGTCCTTTATTTTT
AGGTTCAAGGTTTCATTTGACTTGAGAAAGTGCCCTTCTGCAGCTTCATTGATTTGTTTATC
TTCATAATTAATTGTAACGATTAAAAAGAATAAGAGCACGCAGACCTCTAGGAGAATATTT
TATCCCTGGGTGCCCTGACACATTTATGTAGTGATCCACAAATGTGATTGTTAATTTAAA
TGTTATTCTAATATTAGTACATTGAGTTGTGATGTAATATGAATAACCAGAATCTATTCTT
AAAAGTTTTGAGTATATTTTTCAACTAGATATTTGTATAGAAAGACTGAATAGTGATG

099044.11401

F. W. F. O'NEILL

MGVEIAFASVILTCLSLAAGVSQVLLQPVPTQETGPKAMGDLSCGFAGHS

MGVEIAFASVILTCLSLAAGVSQVLLQPVPTQETGPKAMGDLSCGFAGHS

GGGAATCTGCAGTAGTCTGCCGGCGAATGGAGTGGTGGGCTAGCTGCCGCTCTCGGCTCTGCTGCTGTTGTTCTCTCTGCCCTCAGCGCAGGGCCGCCAGAAGGAGTCAGGTTCAAATGGAAGTATTTATTGACCAAAATTAACAGGTCCTTGGAGAATTACGAACCATGTTCAAGTCAAACGTCAGCTGCTACCATGGTGTCTATAGAAGAGGATCTAACTCCTTCCGAGGAGGCATCTCCAGGAAGATGATGGCAGAGGTAGTCAGACGGAAGCTAGGGACCCACTATCAGATCACTAAGAACAGACTGTACCGGGAAAATGACTGCATGTTCCCTCAAGGTGTAGTGGTGTGAGCACTTTATTTGGAAAGTGATCGGGCGTCTCCCTGACATGGAGATGGTGATCAATGTACGAGATTATCTCTCAGGTTCCATAAATGGATGGAGCCTGCCATCCAGTCTTCTCCTTCAGTAAGACATCAGAGTACATGATATCATGTATCTCTGCTTGGACATTTTGGGAAGGGGGACCTGCTGTTTGGCCAATTTATCCTACAGGTCTTGGACGGTGGGACCTCTTCAGAGAAGATCTGGTAAGGTCAGCAGCACAGTGCCATGGAAAAAGAAAACTCTACAGCATATTTCCGAGGATCAAGGACAAGTCCAGAACGAGATCCTCTCATTTCTTGTCTCGGAAAAACCCAAAACCTGTTGATGCAGAAATACACAAAAACGAGGCTGGAATCTATGAAGATACCTTAGGAAAGCCAGCTGCTCAAGGATGTCATCTTGTGGATCACTGCAAAATACAAGTACTGTTTAATTTTCAGAGCGTAGCTGCAAGTTTCCGGTTATACACCTTCTCTGTGTGGCTCACTTGTTTTCATGTTGGTGATGAGTGGCTAGAATTCTTCATCCACAGCTGAAGCCATGGGTTCACTATATCCAGTCAAAACAGATCTCTCCAATGTCCAAGAGCTGTTACAATTTGTAAGCAAAATGATGATGTAGCTCAAGAGATTGCTGAAAGGGGAAAGCCAGTTATTAGGAACCATTGCGAGATGGATGACATCACCTGTTACTGGGAGAACCTCTTGAGTGAATACTCTAAATTCTGTCTTATAATGTAACGAGAAGGAAAGGTTATGATCAAATTTATCCCAAAATGTTGAAACTGAACATAAGTAGTCATCATAGGACCATAGTCCTCTTTGTGGCAACAGATCTCAGATATCCTACGGTGAGAAGCTTACCATAAGCTTGGCTCCTATACCTTGAATCTGTCTATCAAGCCAAATACCTGGTTTTCTCTATCATGCTGACCCAGAGCAACTCTTGAGAAAGTTTAAATGTGCTAATACACTGATATGAAGCAGTTCACTTTTTGGATGAATAAGGACCAGAAATCGTGAGATGTGGATTTTGAACCAACTCTACCTTTTCATTTTCTTAAGACCAATACAGCTTGTGCCTCAGATCATCCACCTGTGTGAGTCCATCACTGTGAAATTGACTGTGTCCAAGTGTGATGCCCTTTGTCCCATTTTGGAGCAGAAAAATTCGTCATTTGGAAGTAGTACAATCATTGTCTGGAATTGTGAAATTATTCAGGCGTGATCTCTGTCACTTTATTTAATGTAGGAAACCCATGCAATGCAATGATGTAGGAGTCTCTTTGTAAACCATAAACTCTGTGTACTCAGGAGTTTCTATAAATGCCACATGAGAAGAGGCCAAATGTCATGAGTAATTATTGCAATTGGATTGAGGTTCCCTTTTGTGCCTTCATGCCCTACTTCTTAATGCCTCTCTAAAGCCAAA

FIGURE 133

MEWWASSPLRLWLLLFLLPSAQGRQKESGSKWKVFDQINRSLENYEPCCSSQNCSCYHGVE
EDLTPFRGGISRKMMAEVVRRKLGTHYQITKNRLYRENDCMFPSRCSGVEHFILEVIGRLPD
MEMVINVRDYPQVPKWMEPAIPVFSFSKTSEYHDIMYPAWTFWEGGPAVWPIYPTGLGRWDL
FREDLVRSAAQWPWKKNSTAYFRGSRTSPERDPLILLSRKNPKLVDAEYTKNQAWKSMKDT
LGKPAAKDVHLVDHCKYKYLNFNFRGVAASFRFKHLFLCGSLVFHVGDWLEFFYPQLKPWVH
YIPVKTDLSNVQELLQFVKANDDVAQEIAERGSQFIRNHLQMDITCYWENLLSEYSKFLSY
NVTRRKGYDQIIPKMLKTEL

0990040.1140
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FIGURE 134

CACCCCTCCATTCTCGCC**ATG**GCCCTGCATGCTCCTGATCCCTGCTGCCCTCGCCTCTT
TCATCCTGGCCTTTGGCACCGGAGTGGAGTTCGTGCGCTTTACCTCCCTTCGGCCACTTCTT
GGAGGGATCCCGGAGTCTGGTGGTCCGGATGCCCGCCAGGGATGGCTGGCTGCCCTGCAGGA
CCGCAGCATCCTTGCCCCCTGGCATGGGATCTGGGGCTCCTGCTTCTATTGTGTGGGCAGC
ACAGCCTCATGGCAGCTGAAAGAGTGAAGGCATGGACATCCCGGTACTTTGGGGTCTTTCAG
AGGTCACTGTATGTGGCCTGCACTGCCCTGGCCTTGCAGCTGGTGATGCGGTACTGGGAGCC
CATACCCAAAGGCCCTGTGTTGTGGGAGGCTCGGGCTGAGCCATGGGCCACCTGGGTGCCG
TCCTCTGCTTTGTGCTCCATGTCATCTCCTGGCTCCTCATCTTAGCATCCTTCTCGTCTTT
GACTATGCTGAGTCAATGGGCCCTCAAACAGGTATACTACCATGTGCTGGGGCTGGGCAGACC
TCTGGCCCTGAAGTCTCCCCGGGCTCTCAGACTCTTCTCCCACCTGCGCCACCCAGTGTGTG
TGGAGCTGCTGACAGTGTGTGGGTGGTGCTACCTGGGCACGGACCGTCTCCTCCTTGCT
TTCCTCCTTACCCTCTACCTGGGCCCTGGCTCACGGGCTTGATCAGCAAGACCTCCGCTACCT
CCGGGCCAGCTACAAAGAAAACCTCCACCTGCTCTCTCGGCCCCAGGATGGGGAGGCAGAG**T**
GAGGAGCTCACTCTGGTTACAAGCCCTGTTCTTCTCTCTCCACTGAATTCTAAATCCTTAAC
ATCCAGGCCCTGGCTGCTTATGCCAGAGGCCCAATCCATGGACTGAAGGAGATGCCCTT
CTACTACTTGAGACTTTATTCTCTGGGTCCAGCTCCATACCTTAAATCTGAGTTTCAGCCA
CTGAACTCCAAGTCCACTTCTCACCAGCAAGGAAGAGTGGGGTATGGAAGTCATCTGTCCC
TTCAGTGTTTAGAGCATGACACTCTCCCCCTCAACAGCCTCCTGAGAAGGAAAGGATCGCC
CTGACCACTCCCCTGCACTGTTACTTGCCCTCTGCGCCTCAGGGGTCCCCTTGTGACCGCT
GGCTTCCACTCAAGAAGGTGGACAGGGCTTCAAGTTCAACGGTCACTAGTGTCCCTCCA
GGCCCAACCTTGCTCTCACCATCTCCGGGCCCTAGTGTCTGCACTCTTAGGCCCTGCCTCT
GGGCTCAGACCTCCCAACCTAGTCAAGGGGATTCTCCTGCTCTTAACTCGATGACTTGGGGCTC
CCTGCTCTCCCGAGGAAGATGCTCTGCAGGAAAAATAAAGTCAGCCTTTTTCTAAAAAAA

FIGURE 135

MAPALLLIPAALASFILAFGTGVEFVRFTSLRPLLGGIPESGGPDARQGWLAALQDRSILAP
LAWDLGLLLLFVGQHSILMAAERVKAWTSRYFGVLQRSLYVACTALALQLVMRYWEPIPKGPV
LWEARAEPWATWVPLLCFVLHVISWLLIFSILLVFDYAELMGLKQVYYHVLGLGEPLALKSP
RALRLFSLRHPVCVELLTVLWVPTLGTDRLLLAFLLTLYLGLAHGLDQQDLRYLRAQLQR
KLHLLSRPQDGEAE

Signal sequence:

amino acids 1-13

Transmembrane domains:

amino acids 58-76, 99-113, 141-159, 203-222

N-myristoylation sites:

amino acids 37-43, 42-48, 229-235

FIGURE 136

CCGAGCACAGGAGATTGCCCTGCGTTTAGGAGGTGGCTGCGTTGTGGGAAAAGCTATCAAGGA
 AGAAATTGCCAAACCATGTCTTTTTTCTGTTTTTCAGAGTAGTTCCACAACAGATCTGAGTGT
 TTTAATTAAGCATGGAAATACAGAAAACAACAAAAAAGCTTAAGCTTTAATTTTCATCTGGAATT
 CCACAGTTTTCTTAGCTCCCTGGACCCGGTTGACCTGTTGGCTCTTCCCCTGGCTGCTCTA
 TCACGTGGTGTCTCCGACTACTACCCCGAGTGAAAGAACCTTCGGCTCGCGTGCTTCTG
 AGCTGCTGTGGAATGCGCTCTCTGGACTGTCCTTCCGAGTAGGATGTCACTGAGATCC
 CTCAAATGGAGCCTCCTGCTGCTGTCACTCCTGAGTTTCTTTGTGATGTGGTACCTCAGCCT
 TCCCCACTACAATGTGATAGAACGCGTGAAGTGGATGTACTTCTATGAGTATGAGCCGATTT
 ACAGACAAGACTTTCACTTCACACTTCGAGAGCATTCAAAGTCTCTCATCAAAATCCATTT
 CTGGTCATTCTGGTGACCTCCCACCTTCAGATGTGAAAGCCAGGCAGGCCATTAGAGTTAC
 TTGGGGTGAAAAAAGTCTTGGTGGGGATATGAGGTTCTTACATTTTTCTTATTAGGCCAAG
 AGGCTGAAAAGGAAGACAAAATGTTGGCATTGTCTCTAGAGGATGAACACCTTCTTTATGGT
 GACATAATCCGACAAGATTTTTTAGACACATATAATAACCTGACCTTGAAAACCATTTATGGC
 ATTCAGGTGGGTAAGTGGTTTTGCCCCAATGCCAAGTACGTAATGAAGACAGACACTGATG
 TTTTCATCAATACTGGCAATTTAGTGAAGTATCTTTTAAACCTAAACCACTCAGAGAAGTTT
 TTCACAGGTTATCCTCTAATTGATAATTATCCTATAGAGGATTTTACCAAAAAACCATAT
 TTCTTACCAGGAGTATCTTTCAAGGTGTTCCCTCCATACTGCAGTGGGTGGGTTATATAA
 TGCCAGAGATTTGGTGCCAAAGGATCTATGAAATGATGGGTCAAGTAAACCCATCAAGTTT
 GAAGATGTTTTATGTGCGGATCTGTTGAATTTATAAAGTGAACATTATATTCAGAAGA
 CACAAATCTTTCTTCTATATAGAATCCATTTGGATGTCTGTCAACTGAGACGTGTGATTG
 CAGCCCATGGCTTTTCTTCAAGGAGATCATCACTTTTTGGCAGGTCATGCTAAGGAACACC
 ACATGCCATTATTAAGTCTACATTTACAAAAAGCCTAGAAGGACAGGATACCTTGTTGAAA
 GTGTTAAATAAGTAGGTACTGTGAAAATTATGGGGAGGTCAGTGTGCTGGCTTCACTG
 AACTGAACTCATGAAAAACCCAGACTGGAGACTGGAGGTTACACTGTGATTTATTAGTC
 AGGCCCTTCAAAGATGATATGTGGAGGAATTAAATATAAAGGAATTGGAGGTTTTTGTGAAA
 GAAATTAATAGGACCAACAAATTTGGACATGTCACTCTGTAGACTAGAATTTCTTAAAGGG
 TGTTACTGAGTTATAAGCTCACTAGGCTGTAAAAACAAAACAATGTAGAGTTTTATTATTG
 AACAAATGTAGTCACTTGAAGGTTTTGTGTATATCTTATGTGGATTACCAATTTAAAAATATA
 TGTAGTTCTGTGTCAAAAAACTTCTTCACTGAAGTTATACTGAACAAAATTTTACCTGTTTT
 TGGTCATTTATAAGTACTTCAAGATGTTGCAGTATTTACAGTTATTATTATTAAAAATTA
 CTTCAACTTTGTGTTTTTAAATGTTTTGACGATTTCAATACAAGATAAAAAGGATAGTGAAT
 CATTCCTTACATGCAACATTTTCCAGTTACTTAAGTATGAGTTATTATTGATACATCAC
 TCCATTAATGTAAAGTCATAGGTCATTATTGATATCAGTAATCTTGTGGACTTTGTTAAAT
 ATTTTACTGTGGTAAATATAGAGAAGAAATTAAGCAAGAAAATCTGAAA

FIGURE 137

MASALWTVLPSRMSLRSLKWSLLLLLSLSFFVMWYLSLPHYNVIERVNWMYFYEYEPYRQD
FHFTLREHSNCSHQNPFLVILVTSHPSDVKARQAIRVTWGEKKSWWGYEVLTFLLGQEA EK
EDKMLALSLEDEHLLYGDIIHQDFLDYNNLT LKTIMAFRWVTEFCPNAKYVMKTD TDVFIN
TGNLVKYL LNLNHSEKFFTGYPLIDNYSYRGFYQKTHISYQEYPFKVFP PYCSGLGYIMSRD
LVPRIYEMMGHV KPIKFEDVYVGICLNLLKVN IHIPEDTNLFFLYRIHL DVCQLRRVIAAHG
FSSKEIITFWQVMLRNTTCHY

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FIGURE 138

CCTCTGTCCACTGCTTTCGTGAAGACAAGATGAAGTTCACAATTGTCTTTGCTGGACTTCTT
GGAGTCTTTCTAGCTCCTGCCCTAGCTAACTATAATATCAACGTCAATGATGACAACAACAA
TGCTGGAAGTGGGCAGCAGTCAGTGAGTGTCAACAATGAACACAATGTGGCCAATGTTGACA
ATAACAACGGATGGGACTCCTGGAATCCATCTGGGATTATGGAAATGGCTTTGCTGCAACC
AGACTCTTTCAAAGAAGACATGCATTGTGCACAAAATGAACAAGGAAGTCATGCCCTCCAT
TCAATCCCTTGATGCACTGGTCAAGGAAAAGAAGCTTCAGGGTAAGGGACCAGGAGGACCAC
CTCCAAGGGCCTGATGTACTCAGTCAACCCAAACAAAGTCGATGACCTGAGCAAGTTCGGA
AAAAACATTGCAACATGTGTCGTGGGATTCCAACATACATGGCTGAGGAGATGCAAGAGGC
AAGCCTGTTTTTTTACTCAGGAACGTGCTACACGACCAGTGTACTATGGATTGTGGACATTT
CCTTCTGTGGAGACACGGTGGAGACTAAACAATTTTTTAAAGCCACTATGGATTTAGTCAT
CTGAATATGCTGTGCAGAAAAAATATGGGCTCCAGTGGTTTTTACCATGTCAATCTGAAATT
TTTCTCTACTAGTTATGTTTGATTCTTTAAGTTTCAATAAAATCATTAGCATTGAAAAAAA

FIGURE 139

MKFTIVFAGLLGVFLAPALANYNINVNDNNNAGSGQQSVSVNNEHNVANVDNNNGWDSWNS
 IWDYNGGFAATRFLQKKTIVHKMNKEVMPISQSLDALVKEKKLQKGPGGPPPKGLMYSVN
 PNKVDLDSKFGKNIANMCRGIPTYMAEEMQEASLFFYSGTCYTTSVLWIVDISFCGDTVEN

Signal Peptide:

amino acids 1-20

N-myristoylation Sites:

amino acids 67-72, 118-123, 163-168

Flavodoxin protein homology:

amino acids 156-174

FIGURE 140

CATTCTGAACTAATCGTGTGAGAATTGACTTTGAAAAGCATTGCTTTTTACAGAAGTATA
 TTAACTTTTAGGAGTAATTTCTAGTTTGATTGTAATATGAAATAATTTAAAGGGCTTCG
 CTCATATATAGGAAAATCGCATATGGTCTAGTATTAATTTCTTATTGCTTACTGATTTTTT
 TGAGTTAAGAGTTGTTATATGCTAGAATATGAGGATGTGAATATAAATAAGAGAAGAAAAA
 GAATAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAAGCTGGTTTGTTTACATG
 CAAGCTTATAGTTGAAATATTTTTCAGGAATTACATGAATGACAGTCTTCGAACCAATGTGT
 TTGTTTCGATTTCAACCAGAGACTATAGCATGTGCTTGCATCTACCTTGCAGCTAGAGCACTT
 CAGATTCCGTTGCCAACTCGTCCCCATTGGTTTCTTCTTTTTGGTACTACAGAAGAGGAAAT
 CCAGGAAATCTGCATAGAAACACTTAGGCTTTATACCAGAAAAAGCCAACTATGAATTAC
 TGAAAAAAGAAAGTAGAAAAAAGAAAAGTAGCCTTACAAGAAGCCAAATTTAAAGCAAAGGGA
 TTGAATCCGGATGGAACCTCAGCCCTTCAACCCCTGGGTGGATTTTCTCCAGCCTCCAAGCC
 ATCATACCAAGAGAAGTAAAAGCTGAAGAGAAATCACCAATCTCCATTAATGTGAAGACAG
 TCAAAAAAGAACCTGAGGATAGACAACAGGCTTCCAAAAAGCCCTTACAATGGTGTGAAGAAA
 GACAGCAAGAGAAGTAGAAATAGCAGAAGTGAAGTCGATCGAGGTCAAGAACACGATCACG
 TTCTAGATCACATACTCCAAGAAGACACTATAATAATAGCGGAGTCGATCTGGAACATACA
 GCTCGAGATCAAGAAGCAGGTCCCGCAGTCACAGTGAAGCCCTCGAAGACATCATAATCAT
 GGTTCTCCTCACCTTAAGGCCAAGCATACCAGAGATGATTTAAAAAGTTCAAACAGACATGG
 TCATAAAAGGAAAAAATCTCGTTCTCGATCTCAGAGCAAGTCTCGGGATCACTCAGATGCAG
 CCAAGAAACACAGGCATGAAAGGGGACATCATAGGGACAGGCGTGAACGATCTCGCTCCTTT
 GAGAGGTCCCATAAAAAGCAAGCACCATGGTGGCAGTCGCTCAGGACATGGCAGGCACAGGCG
 CTGAATTTCTCTTCTTTGAGCCTGCATCAGTTCTTGGTTTTGCCTATCTACAGTGTGATGT
 ATGGACTCAATCAAAACATTAAACGCAAACTGATTAGGATTGATTCTTGAACCCCTCTA
 GGTCTCTAGAACACTGAGGACAGTTTCTTTTGAAGAAGTATGTTAATTTTTTGCACATT
 AAAATGCCCTAGCAGTATCTAATAAAAACCATGGTCAGGTTCAATTGTACTTTATTATAGT
 TGTGTATTGTTTATTGCTATAAGAACTGGAGCGTGAATCTCTGAAAAATGTATCTTATTTTT
 ATACAGATAAAATTGCAGACACTGTTCTATTTAAGTGGTTATTGTTTAAATGATGGTGAAT
 ACTTTCTTAACACTGGTTTGTCTGCATGTGTAAGAGATTTTACAAGGAATAAAATACAAAT
 CTTGTTTTTTCTAAAAAAGG

FIGURE 141

MNDSLRTNVFVRFPETIACACIYLAARALQIPLPTRPHWFLFLFGTTEEEIQEICIETLRLY
TRKKPNYELLEKEVEKRRVALQEAKLKAKGLNPDGTPALSTLGGFSPASKPSSPREVKAEK
SPISINVKTVKKEPEDRQQASKSPYNGVRKDSKRSRNSRSASRSRSRTRSRSRSHTPRRHYN
NRRSRSGTYSSRSRSRSHSESPRRHHNHGSPHLKAKHTRDDLKSNRHGHKRRKRSRSQ
SKSRDHSDAAKKHRHERGHHRDRRERSRSFERSHKSKHHGGSRSGHGRHRR

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FIGURE 142

TGGGGATAAAGGAAAAATGGTCAGGTATTAATGGCTTAAAGATTATTGGAAGGGGTTTATCA
TTTTTTGAANNATATCGGGTCANAATTGNCTTTGAAAAGCATTGCTTTTTACAGAAATATAT
TANCTTTTAGAGTAATTTCTAGTTTGGATTGTAATATGAAATTATTTAAAAGGGCTTCGCT
CATATATAGGAAAATCGCATATGGTCCTAGTATTAAATTNTTATTGCTTACTGATTTTTTTTG
AGTTAAGAGTTGTTATATGNTAGAATATGAGGATGTGAATATAAATAAGAGAAGAAAAAGA
ATAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAACTGGTTTGTTCATGCA
AGCTTATAGTTGAAATATTTTCAGGAATTACATGAATGACAGTCTTCGAACCAATGTGTTT
GTTCGATTTCAACCAGAGANTATAGCATGTGCTTGCATCTACCTTGCAGNTAGAGCACTTCA
GATTCGGTTGCCAACTNGTCCCCATTGGTTTCTTCTTTTTTGGTACTACAGAAGAGGAAATCC
AGGAAATNTGCATAGAAACACTTAGGCCTTTATACCAGAAAAAGCCAAACTATGAATTACTG
GAAAAAGAAGTAGAAAAAGAAAAGTAGCCTTACAAGAAGCCNAATTAAGCAAAGGGATT
GAATCCGGATGGAATCCAGCCCTTTCAACCCTGGGTGGATTTCCTCC

TCTTCTGGGTTT

FIGURE 143

GGCACGAGGCTCGTGCCAAAGCTTGGCACGAGGGTGCACCGCTTCTCGCACGCGT**CATGGC**
GGTCCTCGGAGTACAGCTGGTGGTGACCCCTGCTCACTGCCACCCCTCATGCACAGGCTGGCGC
CACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAAACGGCAGTTTGTTCGGATACAAGCACCCG
TCTGAGGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCCAGAGGCAGGAAAGAGCGGTG
GGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCCGAGATGCCCCGTTCCAGCTGG
AGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCTGCGCTTCTTCTGAGATACCACTGG
TTTGTGGACTTTGCTGTGTAAGTGGCGCGGTGTACCTCTTACAGAGGCCTACTACTACAT
GCTGGGACCAAGCAAGGAGACTAACATTGCTGTGTTCTGGTGCCTGCTCACGGTGACCTTCT
CCATCAAGATGTTCTGACAGTGACACGGCTGTACTTCAAGCGCCGAGGAGGGGGGTGAGCGC
TCTGTCTGCCTCACCTTTGCCCTTCTTCTGCTGCTGGCCATGCTGGTGCAAGTGGTGGC
GGAGGAGACCTTCGAGCTGGGCCTGGAGCCTGGTCTGGCCAGCATGACCCAGAAGCTTAGAGC
CACTTCTGAAGAAGCAGGGCTGGGACTGGGCGCTTCTGTGGCCAAGCTGGCTATCCGCGTG
GGACTGGCAGTGGTGGGCTCTGTGCTGGGTGCCCTTCCACCTTCCCAGGCCCTGGCGCTGGC
CCAGACCCACCGGACGCACTGACCATGTGCGAGGACAGACCCATGCTGCAGTTCTTCTCTGC
ACACAGCTTCTGTCTCCCCGTTCATCCTGTGGCTCTGGACAAAGCCATTGCACGGGAC
TTCTGCAACAGCCGCGCTTTGGGGAGACGCTTTCTCCCTGCTGTCCGATTCTGCCTTCGA
CTCTGGGCGCCTCTGGTTGCTGGTGGTGCTGTGCTGCTGCGGCTGGCGGTGACCCGGCCCC
ACCTGCAGGCCCTACCTGTGCCTGGCCAAGGCCCGGGTGGAGCAGCTGCGAAGGGAGGCTGGC
CGCATCGAAGCCCGTGAAATCCAGCAGAGGTGGTCCGAGTCTACTGCTATGTGACCGTGGT
GAGCTTGCACTACCTGACGCCGCTCATCCTCACCCCTCAACTGCACACTTCTGCTCAAGACGC
TGGGAGGCTATTCTGGGGCCTGGGCCAGCTCCTTACTATCCCCGACCCATCCTCAGCC
AGCGCTGCCCCCATCGGCTCTGGGGAGGACGAAGTCCAGCAGACTGCAGCGCGGATTGCCGG
GGCCCTGGGTGGCCTGCTTACTCCCCCTTCTCCTCGTGGCGTCTGGCCTACCTCATCTGGT
GGACGGCTGCCTGCCAGCTGCTGCCAGCCTTTTCGGCCTCTACTTCCACAGCACTTGGCA
GGCTCC**TAG**CTGCCTGCAGACCTCCTGGGGCCCTGAGGTCTGTCTGGGGCAGCGGGACA
CTAGCCTGCCCCCTCTGTTTGGCGCCCCGTGTCCCAGCTGCAAGGTGGGGCCGGACTCCCC
GGCGTTCCCTTACACAGTGCCCTGACCCGCGGCCCCCTTGGACGCCGAGTTTCTGCCTCA
GAACTGTCTCTCTGGGCCAGCAGCATGAGGGTCCCGAGGCCATTGTCTCCGAAGCGTATG
TGCCAGGTTTGGTGGCGAGGGTGATGCTGGCTGCTCTTCTGAACAAATAAAGGAGCATGCC
GATTTTTAA

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MAVLGVQLVVTLLTAPLMHRLAPHCSFARWLLCNGSLFRYKHPSEELRALAGKPRPRGRKE
RWANGLSEEKPLSVPRDAFFQLETCLPTTVDALVLRFFLEYQWVFDAVYSGGVYLFT EAYY
YMLGPAKETNIAVFWCLLTVTFSIKMFLTVRTRYPSAEEGGERSVCLTFATFLLLAMLVQV
VREETLELGLPEGLASMTQNLEPLLKKQGDWALPVAKLAIRVGLAVVGSVLGAFTLPFGLR
LAQTHRDALTMSEDRPMLQFLLHTSFLSPLFILWLWTKPIARDFLHQPPFGGETRFSLLSDSA
FDSGRLLWLLVVLCLLR LAVTRPHLQAYLCLAKARVEPLLRREAGRIEAREIQQRVVRVYCVYT
VVSQYLTLPLILNTCLLTLLKGYSGWGLGPAQLSPDRESSAIAPIGSGBEVDQQTAAIRI
AGALGGLLTLPFLRGVLAIVLWWTAACOLLASLFGLYFHOHLAAS

FIGURE 145

CGTTNGCACGCGTCAATGGCGGTCCTCGGAGTACAGCTGGTGGTGACCCTGCTCACTGCCAC
CCTCATGCACAGGCTGGCGCCACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAACGGCAGTT
TGTTCCGATACAAGCACCCGTNTTGAGGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCC
CAGAGGCAGGAAAAGAGCGGTGGGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCC
GAGATGCCCCGTTCCAGCTGGAGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCTGCGC
TTCTTCCTGGAGTACCAGTGGTTTGTGGACTTTGCTGTGTACTCGGGCGGCGTGTACCTCTT
CACAGAGGCCTACTACTACATGCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTGGT
GCCTGCTCACAGTGACCTTCTCCATCAAGATGTTCTGACAGTGACACGGCTGTACTTCAGC
GCCGAGGAGGGGGGTGAGCGCTCTGTCTGCCTCACCTTTGCCTTCCTCTTCCTGCTGCTGGC
CATGCTGGTGCAAGCG

FIGURE 146

GGTTCCTACATCCTCTCATCTGAGAATCAGAGAGCATAATCTTCTTACGGGCCCCGTGATTATTAAACGTGGCTT
 AATCTGAAGGTTCTCAGTCAAAATCTTTGTGATCTACTGATTGTGGGGGCATGCGCAAGGTTTGCTTTAAAGGAGC
 TTGGCTGGTTTGGGCCCTTGTAGCTGCACAGAAGGTGGCCAGGGAGAATGCAGCACATCTGCTCGGAGAAATGAAGG
 CGCTTCTGTTGCTGGCTTGGCTTGGCTCAGTCTCTGCTAATACATTGACAATGTGGGCAACCTGCACCTTCTCTG
 TATTTCAGAACTCTGTAAAGTGCCTCCCACTACGGCTGACCAAGATAGGAAGAGGCGCTCACAGATGGCTG
 TCCAGACGGCTGTGCGAGCCTCACAGCCACGGCTCCCTCCCCAGAGGTTTCTGCGAGCTGCCACCATCTCCTTAA
 TGACAGACGAGCCTGGCTTACACAACCTCGCTACGTGTCTCGGAGAGGACGGGCTGCGAGCAATCAGCCCA
 GTGGACTCTGGCCGGAGCAACCGAATAGGGCACGGCCCTTTGAGAGATCCACATATTAGAAGCAGATCATTTAA
 AAAAATAAATCGAGCTTTGAGTCTTCTCGAAGGACAAAGAGCGGGAGTGCAGTTGCCAACCATGCCAGCAGG
 GCAGGGAAATTTCTGAAACACCACTGCCCTGAAGTCTTTCCAGGTTGTACCACTGATTCCAGATGGTGAA
 ATTACAGCATCAAGATCAATCGATAGATCCAGTGAAGCCTCTCTATTAGGCTGGTGGGAGTAGCGGAAC
 CCCACTGGTCCATATCATTTATCCAACACATTTATCTGATGGGTGATCGCCAGAGAGCGCCGCCTACTGCCAG
 GAGACATCATTTCAAAGGTCAACGGGATGGACATCAGCAATGTCCCTCACAACCTACGCTGTGCGTCTCCTGCGG
 CAGCCCTGCCAGGTGCTGTGGCTGACTGTGATGCGTGAACAGAAAGTTCCGCGAGCAGGAACAATGGACAGGCC
 GGATGCCACAGACCCCGAGATGACAGCTTTCATGTGATTTCTCAACAAAAGTAGCCCCGAGGAGCAGCTTGGAA
 TAAAACCTGGTGGCAAGGTGGATGAGCCTGGGTTTTATCTTCAATGTGCTGGATGGCGGTGTGGCATATCGA
 CATGGTCAGCTTGAGGAGAATGACCGTGTGTAGCCATCAATGGACATGATCTTCGATATGGCAGCCCAAGAA
 TGGCGTCTATCTGATTGAGGCCAGTGAAGACGTGTTCACTCGTGTGCCGACAGGTTCGGCAGCGGAGCC
 CTGACATCTTTCAGGAAGCCCGCTGGAACAGCAATGGCAGCTGGTCCCCAGGGCCAGGGGAGAGGAGCAACAT
 CCCAAGCCCTCCATCTCAATTTACTTGTTCATGAGAAGGTGGTAAATATCCAAAAGACCCCGGTGAATCTCT
 CGGCATGACCGTCCGAGGGGGAGCATCACATAGAGAATGGGATTTGCCATCTATGTCTCAGTGTGAGCCCG
 GAGGAGTCATAAGCAGAGATGGAAGAATAAAAACAGGTGACATTTTGTGAATGTGGATGGGGTGAAGTGA
 GAGGTGAGCGGAGTGAGGAGTGCCATATTGAAAGAAACATCATCCTCGATAGTACTCAAAGCTTTGGAAGT
 CAAAGAGTATGAGCCCGAGGAAGACTGCAGCAGCCAGCAGCCCTGGAATCCAAACCAACATGGCCCCACCCA
 GTGACTGGTCCCCATCTCGGTGATGTGGTGGAAATTACACCGTGCTTGTATACATGTAAGATATTGTATTA
 CGAAGAAACACAGCTGGAAGTCTGGGCTTCTGCATTGTAGGAGGTTATGAAGAATACAATGGAACAAACCTTT
 TTTTCATCAATCCATTTGTTGAAGGAACACCAAGCATACATGATGAAGAATAGATGGTGATATTTCTCTTG
 CTGTCAATGGTAGAAGTACATCAGGAATGATACATGCTTGTCTGGCAAGACTGGTGAAGAAGCTTAAAGGAAGA
 ATTACTCTAATATTGTTTCTGGCCTGGCACTTTTTATAGAAATCAATGATGGGTGAGAGGAAACAGAAAAA
 TCACAAATAGGCTAAGAAGTTGAACACTATATTTATCTTGTGAGTTTTATATTAAAGAAAGAAATACATTTG
 AAAAATCTAGGAAAGTATGATCTCTAATGAAGCCAGTTACACCTCAGAAATATGATTCCAAAAAATTA
 AAACCTAGTATTTTTTTTTCAGTGTGGAGGATTTCTCATCTCTACAACATGTGTTATTTTTTTCTATTCAAT
 AAAAGCCCTAAACACTCAAAATGATTGATTGTATACCCCATGAATTCAGCTGATTAAATTTAAATTT
 GGTATATGCTGAAGTCTGCCAAGGTACATATTGGCCATTTTAAATTTACAGCTAAATATTTTTTAAATGCA
 TTGCTGAGAAACGTTGCTTTCATCAACAGAATAAAATATTTTCAGAAGTTAA

FIGURE 147

MKALLLLVLPWLS PANYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGC PDGCASLTAT
APSPEVSAAATISLMTDEPGLDNPAYVSSAEDGQPAISPVD SGRSNRTRARPFERSTIRSRS
FKKINRALSVLRRTKSGSAVANHADQGRESENTTAP EVFPRLYHLIPDGEITSIKINRVDP
SESLSIRLVGGSETPLVHII IQHIYRDGVIARDGRLLPGDIILKVNGMDISNVPHNYAVRLL
RQPCQVLWLTVMREQKFRSRNNGQAPDAYRPRDDSFHVILNKSSPEEQLG IKLVRKVDEPGV
FIFNVLDGGVAYRHGQLEENDRVLAINGHD LRYGSPESA AHLIQASERRVHLVVS RQVRQRS
PDIFQEAGWNSNGSWSPGPGERSNTPKPLHPTITCHEKV VNIQKDPGESLGMTVAGGASHRE
WDLPIYVISVEPGGVISRDGRIKTDILLNVDGVELTEVSRSEAVALLKRTSSSIVLKALEV
KEYEPQEDCSSPAALDSNHNMAPPSDWSPSWVMWLELPRCLYNCKDIVLRNRTAGSLGFCIV
GGYEEYNGNKPF FIKSIVEGTPAYNDGRIRCGDILLAVNGRSTSGMIHACLARLLKELKGRI
TLTIVSWPGTFL

147-040660

FIGURE 148

CCAAAGTGATCATTTGAAAAAGAGATATCCACATCTTCAAGCCCATATAAAGGATAGAAGCT
GCACAGGGCAGCTTTACTTACTCCAGCACCTTCCTCTCCCAGGCAAATGGTGTGCTGACCATCT
TTGGGATACAATCTCATGGATACGAGGTTTTTAACATCATCAGCCCAAGCAACAATGGTGGC
AATGTTTCAGGAGACAGTGACAATTGATAATGAAAAAATACCGCCATCGTTAACATCCATGC
AGGATCATGCTCTTCTACCACAATTTTTGACTATAAACATGGCTACATTGCATCCAGGGTGC
TCTCCCGAAGAGCCTGCTTTATCCTGAAGATGGACCATCAGAACATCCCTCCTCTGAACAAT
CTCCAATGGTACATCTATGAGAAACAGGCTCTGGACAACATGTTCTCCAACAAATACACCTG
GGTCAAGTACAACCTCTGGAGTCTCTGATCAAAGACGTGGATTGGTTCCTGCTTGGGTCAC
CCATTGAGAACTCTGCAAACATATCCCTTTGTATAAGGGGGAAGTGGTTGAAAACACACAT
AATGTCGGTGCTGGAGGCTGTGCAAAGGCTGGGCTCCTGGGCATCTTGGGAATTTCAATCTG
TGAGACATTATGTTTAGGATGATTAGCCCTCTTGTTTTATCTTTCAAAGAAATACATCC
TTGGTTTACACTCAAAAGTCAAATTAAATTCTTTCCCAATGCCCAACTAATTTTGAGATTC
AGTCAGAAAATATAAATGCTGTATTATA

MKILVAFLVLTIFGIQSHGYEVFNIISPSNNGGNVQETVTIDNEKNTAIVNIHAGSCSST
 IFDYKHGYIASRVLSRRACFILKMDHQNIPLNNLQWYIYEKQALDNMFSNKYTWVKYNPLE
 SLIKDVDWFLGSPIEKLCKHIPLYKGEVVENTHNVGAGGCAGLGLGILGISICADIHV

FIGURE 150

GGCACGAGCCAGGAAGTCTGAGGTTCTCACTGCCGAGCAGAGGCCCTACACCCACCGAGGC
ATGGGGCTCCCTGGGCTGTTCTGCTTGGCCGTGCTGGCTGCCAGCAGCTTCTCCAAGGCACG
GGAGGAAGAAATTACCCCTGTGGTCTCCATTGCCTACAAAGTCTTGGAAAGTTTCCCCAAAG
GCCGCTGGGTGCTCATAACCTGCTGTGCACCCAGCCACCACCGCCCATCACCTATTCCCTC
TGTGGAACCAAGAACATCAAGGTGGCCAAGAAGGTGGTGAAGACCCACGAGCCGGCCTCCTT
CAACCTCAACGTCACTCAAGTCCAGTCCAGACCTGCTCACCTACTTCTGCCGGGCGTCCT
CCACCTCAGGTGCCCATGTGGACAGTGCCAGGCTACAGATGCACTGGGAGCTGTGGTCCAAG
CCAGTGTCTGAGCTGCGGGCCAACTTCACTCTGCAGGACAGAGGGGCAGGCCCCAGGGTGGA
GATGATCTGCCAGGCGTCTCGGGCAGCCACCTATCACCAACAGCCTGATCGGGAAGGATG
GGCAGGTCCACCTGCAGCAGAGACCATGCCACAGGCAGCCTGCCAACTTCTCCTTCTGCCG
AGCCAGACATCGGACTGGTTCTGGTGCCAGGCTGCAACAACGCCAATGTCCAGCACAGCGC
CCTCACAGTGGTGCCCCAGGTGGTGACCAGAAGATGGAGGACTGGCAGGGTCCCCCTGGAGA
GCCCCATCCTTGCCCTGCCGCTCTACAGGAGCACCCGCCGTCTGAGTGAAGAGGAGTTGGG
GGGTTTCAAGATAGGGAATGGGGAGGTCAGAGGACGCAAAGCAGCAGCCATG**TAG**AATGAACC
GTCCAGAGAGCCAAGCACGGCAGAGGACTGCAGGCCATCAGCGTGCACTGTTCTGATTTGGA
GTTTATGCAAAATGAGTGTGTTTGTAGCTGCTCTTGCCACAAAAAAAAAAAAAAAAAAAAA

FIGURE 151

MGLPGLFCLAVLAASSFSKAREEEITPVVSIAYKVLEVFPKGRWVLITCCAPQPPPPITYSL
CGTKNIKVAKKVVKTHEPASFNLVTLKSSPDLLTYFCRASSTSGAHVDSARLQMHWELWSK
PVSELNANFTLQDRGAGPRVEMICQASSGSPFITNSLIGKDGQVHLQQRPCHRPANFSFLP
SQTSDWFWCQAANNANVQHSALTVPVPPGGDQKMEDWQGPLESPIALPLYRSTRRLSEEEFG
GFRIGNGEVRGRKAAAM

Signal Peptide:

amino acids 1-18

N-glycosylation Sites:

amino acids 86-89, 132-135, 181-184

GGTCTCTTAATGCGCAGCAGCCGCCGCTACCAAGATCCTTCTGTGCCTCCCGCTTCTGCTCCTG
CTGTCCGGCTGGTCCCGGGCTGGGCGAGCCGACCCTCACTCTCTTTGCTATGACATCACCGT
CATCCCTAAGTTCAGACCTGGACCACGGTGGTGTGCGGTTCAAGGCCAGGTGGATGAAAAGA
CTTTTCTTCACTATGACTGTGGCAACAAGACAGTCACACCTGTCAGTCCCTGGGGAGAAGAA
CTAAATGTCAACAGCGCTGGAAAGCACAGAACCAGTACTGAGAGAGGTGGTGGACATACT
TACAGAGCAACTGCGTGACATTCACTGGAGAATTACACACCCAAGGAACCCCTCACCCTGC
AGGCAAGGATGTCTTGTGAGCAGAAAGCTGAAGGACACAGCAGTGGATCTTGGCAGTTTCAGT
TTCGATGGGCAGATCTTCCTCCTCTTTGACTCAGAGAAGAGAAATGGGACAACGGTTCATCC
TGGAGCCACAAGATGAAAGAAAAGTGGGAGAAATGACAAGGTGTGGCCATGTCCTTCCATT
ACTTCTCAATGGGAGACTGTATAGGATGGCTTGAGGACTCTTGTATGGGCATGGACAGCACC
CTGGAGCCAAGTGCAGGAGCACCACCTCGCCATGTCTCAGGCACAACCCAACCTCAGGGCCAC
AGCCACCACCCCTCATCCTTTGCTGCCTCCTCATCATCTCCCTGCTTCATCCTCCCTGGCA
TCTGAGGAGAGTCTTTAGAGTGACAGGTTAAAGCTGATACCAAAGGCTCCTGTGAGCAG
GTCTTGATCAAATCGCCCTTCTGTCTGGCCAGCTGCCACGACCTACGGTGTATGTCCAGT
GGCCTCCAGCAGATCATGATGACATCATGGACCCAATAGCTCATTCAGTGCCTTGATTCTT
TTGCCAACAAATTTACCAGCAGTTATACCTAACATATTATGCAATTTTCTCTTGGTGCTACC
TGATGGAATTCCTGCACTTAAAGTTCTGGCTGACTAAACAAGATATATCATTTTCTTTCTTC
TCTTTTGTTTGGAAAATCAAGTACTTCTTTGAATGATGATCTCTTTCTGCAAATGATATT
GTCAGTAAATAATACCGTTAGACTTCAGACCTCTGGGAATCTTTCCGTGTCCTGAAAGAG
AATTTTAAATTTAATAAGAAAAAATTTATATTGATGATTGTTTCCCTTTAGTAAATTTAT
TGTTCTGTACTGATATTTAAATAAGAGTTCTATTTCACCAAAAAAAAAAAAAAAAAAAAA

FIGURE 153

MAAAATKILLCLPLLLLLSGWSRAGRADPHSLCYDITVIPKFRGPRWCAVQGQVDEKFTL
HYDCGNKTVTPVSPLGKKNVTAWKAQNVLREVVLDLTEQLRDIQLENYTPKEPLTLQAR
MSCEQKAEGHSSGSWQSFSDGQIFLLFDSEKRMWTVHPGARMKEKEWENDKVVAMSIFYFS
MGDCIGWLEDFLMGMDSTLEPSAGAPLAMSSGTTQLRATATTLILCCLLIILPCFILPGI

Important features:

Signal peptide:

amino acids 1-25

Transmembrane domain:

amino acids 224-246

N-glycosylation site.

amino acids 68-72, 82-86

N-myristoylation site.

amino acids 200-206, 210-216

Amidation site.

amino acids 77-81

FIGURE 154

GGGAAAGCCATTTGAAAACCCATCTATACAACTATATATTTTCATTTCTGCTGCTAGCTG
CCTTGGGCCTCACAATTTTCATTTCTGTTTCTGACTTTCAAGTTATATACCGTGGAAATGGAG
TTGATCCCAACCATAACATCGTGGAGGGTTTTAATTTGGTGGTAGCCCTCACCCAATTCG
GTGTGGCTTTCTTTCAGAGGATTCCACCTTCAAAATCATGAACTCTGGCTGTTGATCAAAA
GAGAATTTGGATTCTACTCTAAAAGTCAATATAGGACTTGGCAAAAGAAGCTAGCAGAAGAC
TCAACCTGGCCTCCCATAAACAGGACAGATTATTCAGGTGATGGCAAAAATGGATTCTACAT
CAACGGAGGCTATGAAAGCCATGAACAGATTCCAAAAAGAAAACCAAATTGGGAGGCCAAC
CCACAGAACAGCATTTCTGGGCCAGGCTGTAAATCAGAATTGTCGTCGTACATGCTCAACAGC
ATTGCTTTTTTCCCCAAAATTAACACATTGTGGAGAAGTGATGATACTCTCCCCTTACCTTT
CCTCTCTCCATTCAAGCATTCAAAGTATATTTTCAATGAATTAACCTTGCAGCAAGGGACC
TTAGATAGGCTTATTCTGACTGTATGCTTTACCAATGAGAGAAAAAATGCATTTCTGTAT
CATCCTTTTCAATAAACTGTATTCAATTTGAAAAAAAAAAAAAAAAAAAAA

CCGCGGCG 11401

155/330

FIGURE 155

MELIPTITSWRVLILVVALTQFWCGFLCRGFHLQNHFWLLIKREFGFYSKSQYRTWQKKLA
EDSTWPPINRTDYSGDGKNGFYINGGYESHEQIPKRKLKLGQPTEQHFWARL

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FIGURE 156

GTTCTCCTTTCCGAGCCAAAAATCCAGGCGATGGTGAATTATGAACGTGCCACACCA**ATGAAG**
 CTCTTGTGGCAGGTAAC**TGTG**CACCACCACACCTGGAATGCCATCCTGCTCCCGTTTCGTCTA
 CCTCACGGGCGCAAGTGTGGATTCTGTGTGCAGCCATCGCTGCTGCCGGCTCAGCCGGGCCCC
 AGAACTGCCCTCCGTTTGTCTCGTGCAGTAACCAAGTT**CAGCA**AGGTGGTGTGCACGCGCCGG
 GGCTCTCCGAGGTCCCGCAGGGTATTCCTCGAACACCCGGTACCTCAACCTCATGGAGAA
 CAACATCCAGATGATCCAGGCCGACACCTTCCGCCACCTCCACCACCTGGAGGTCCTGCAGT
 TGGGCAGGAACCTCCATCCGGCAGATTGAGGTGGGGCCCTTCAACGGCTGGCCAGCCTCAAC
 ACCCTGGAGCTGTTTCGACAACTGGCTGACAGT**CATCC**TAGCGGGGCCCTTTGAATACCTGTC
 CAAGCTGCGGGAGCTCTGGCTTCGCAACAACCCATCGAAAGCATCCCTCTTACGCCCTCA
 ACCGGGTGCCCTCCCTCATGCGCCTGGACTTGGGGGAGCTCAAGAAGCTGGAGTATATCTCT
 GAGGGAGCTTTTGGGGGCTGTTCAACCTCAAGTATCTGAACTTGGGCATGTGCAACATTAA
 AGACATGCCCAATCTCACCCCTGGTGGGGCTGGAGGAGCTGGAGATGT**CAGGGA**ACCCT
 TCCCTGAGATCAGGCCTGGCTCCTTCCATGGCTGAGCTCCCTCAAGAAGCTCTGGGTCATG
 AACTCACAGGTACGCCCTGATTGAGCGGAATGCTTTGACGGGCTGGCTTCACTTGTGGAAC
 CAACTTGGCCCAACAATAACCTCTCTTCTTGGCCCATGACCTCTTTACCCCGCTGAGGTACC
 TGGTGGAGTTGCATCTACACCACAACCTTGGAACTGTGATTGTGACATTCTGTGGCTAGCC
 TGGTGGCTTCGAGAGTATATACCCACCAATTCACCTGCTGTGGCCGCTGT**CA**TGCTCCCAT
 GCACATGCGAGGGCCGCTACCTCGTGGAGGTGGACCAGGCCCTCCTTCCAGTGCCTGCGCCCT
 TCATCATGGAGCGACCTCGAGACCTCAACATTCTGAGGGTCCGATGGCAGAACTTAAAGTGT
 CGGACTCCCCCTATGTCTCCGTGAAGTGGTGTCTGCCCCAATGGGACAGTGTCTCAGCCACGC
 CTCCCGCCACCAAGGATCTCTGTCTCAACGACGGCACCTTGAAC**TTTTCC**ACAGTGTCTGC
 TTTCAGACACTGGGGTGTACACATGCATGGTGACCAATGTTGCAGGCAACTCCACGCCTCG
 GCCTACCTCAATGTGAGCACGGCTGAGCTTAACACCTCCAAC**TACAGCTTCTT**CACCACAGT
 AACAGTGGAGACCACGGAGATCTCGCCTGAGGACACAACGCGAAAGTACAAGCCTGTTCTTA
 CCAGTCCACTGGTTACCAGCCGGCATATACCACCTTACCACGGTGTCTCATT**CAGACT**ACC
 CGTGTGCCCAAGCAGGTGGCAGTACCCGCGACAGACACCCTGACAAGATGCAGACAGGCCT
 GGATGAAGTCATGAAGACCACCAAGATCATCATTGGCTGCTTGTGGCAGTGACTCTGTAGT
 CTGCCGCCATGTTGATTGTCTTCTATAAACTTCGTAAGCGGCACCAGCAGCGGAGTACAGTC
 ACAGCCGCCCGGACTGTTGAGATAATCCAGGTGGACGAAGACATCCAGCAGCAACATCCGC
 AGCAGCAACAGCAGCTCCGTCCGGTGTATCAGGTGAGGGGCGAGTGTCTGCCCA**CAATTC**
 ATGACCATATTAAC**TACA**ACACCTACAAACCCAGCACATGGGGCCCACTGGACAGAAAAACAGC
 CTGGGAAGCTCTCTGCACCCACAGTCACCACATCTCTGAACCTTATATAATT**CAGACCCA**
 TACCAAGGACAAGGTACAGGA**AACTCAA**ATATGA**CTCC**CTCCCCCAAA**AACTTATA**AAAT
 GCAATAGAATGCACACAAAGACAGCAACTTTTGTACAGAGTGGGAGAGACTTTTCTTGTGA
 TATGCTTATATATTAAGCTATGGGCTGGTTAAAAAAACAGATTATATTAA**AAATTA**AGA
 CAAAAAGTCAAAAA

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FIGURE 157

MKLLWQVTVHHHTWNAILLPFVYLTAQVWILCAAIAAASAGPQNCPSVCSCSNQFSKVVCT
RRGLSEVPQGI PSNTRYLNLMENNIQMIQADTFRHLHHLEVLQLGRNSIRQIEVGAFNGLAS
LNTLELFDNWLTVIPSGAFEYLSKLRELWLRNNPIESIPSYAFNRVPSLMRLDLGELKKLEY
ISEGAFEGFLNLYNLGMCNIKDMPNLTPLVGLEBLEMSGNHFFPEIRPGSFHGLSSLKKLW
VMNSQVSLIERNAFDGLASLVELNLAHNNLSSLPHDLFTPLRYLVELHLHNPWNCDCDILW
LAWWLREYIPTNSTCCGRCHAPMHMRGRYLVEVDQASFOCSAPFIMDAPRDLNISEGRMAEL
KCRTPPMSSVKWLLPNGTVLSHASRHRISVLNDGTLNFSHVLLSDTGVYTCMVTNVAGNSN
ASAYLNVSTAE LN TSNYSFFT VTVETTEISPEDTTRKYKVPVTTSTGYQPAYTTSTTVLIQ
TTRVPKQVAVPATDTTDMQTSLDEVMTTKIIIGCFVAVTLLAAAMLIVFYKLRKRHQQRS
TVTAARTVEIIQVDEDIPAATSAAATAAPSGVSGEGAVVLPTIHDHINYNTYKPAHGAHWTE
NSLGNLHPTVTTTISEPYIIQTHTKDKVQETQI

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FIGURE 158

CGCTCGGGACCAGCCGCGGCAAGGATGGAGCTGGGTGCTGGACGAGTTGGGGCTCAGTTTCTTCAGCTCC
 TTCTCATCTCGCTCTGCCAAGAGAGTACACAGTCATTAAATGAAGCCTGCCTTGAGCAGAGTGGAAATATCATG
 TGTGCGGAGTGTGTAATATGATCAGATTGAGTGCCTGCCCCGGAAAGAGGGAAGTCGTGGGTATATACCAT
 CCCTTGCTCGAGGAATGAGGAGAAATGAGTGTGACTCCTGCCTGATCCACCCAGGTTGTACCATCTTTGAAAACT
 GCAAGAGCTGCCCAGAAATGGCTCATGGGGGGTACCTTGGATGACTTCTATGTGAAGGGGTTCATCTGTGAGAG
 TGCCGAGCAGGCTGGTACGGAGGAGACTGCATGCGATGTGGCCAGGTTCTGCGAGCCCCAAGGGGTGAGATTAA
 GTTGGAAAGCTATCCCCAAATGCTCCTCACTGTGAATGGACCATTCATGCTAAACCTGGGTTTGTCTCATCCAACTT
 GATTGTGTCATGTTGAGTCTGGAGTTTGACTACATGTGCCAGTATGACTATGTTGAGGTTGCTGATGGAGACAAC
 CGCAGTGGCCAGATCATCAAGCTGTCTGTGGCAACGAGCGGCCAGCTCCTATCCAGAGCATAGGATCCTCACT
 CGCGTCCCTCTTCCACTCGATGGCTCCAAGAAATTTGACGGTTTCCATGCCATTTATGAGGAGATCACAGCAT
 GCTCCTCATCCCCCTGTTTCCATGACGGCACGTGCGTCTTGACAAGGCTGGATCTTACAAGTGTGCTGCTTG
 GCAGGCTATACTGGGCGAGCGCTGTGAAAATCTCCTTGAAGAAAGAACTGCTCAGACCCCTGGGGGCCAGTCAA
 TGGGTACAGAAAAATAACAGGGGGCCCTGGGCTTATCAACGGACGCCATGCTAAAATTGGCACCCGTGGTGTCTT
 TCTTTTGTAACAACTCCTATGTTCTTAGTGGCAATGAGAAAAGAACTTGCCAGCAGAAATGGAGAGTGGTCAGGG
 AAACAGCCCATCTGCATAAAAGCCTGCGCAGAGAACCAAGATTTGAGACCTGGTGAGAAAGGAGAGTTCTTCCGAT
 GCAGGTTTCAGTCAAGGGAGACACCATTACACCGACTATACTCAGCGGCTTCAGCAAGCAGAAATGCAAGAGTG
 CCCCTACCAAGAAGCGACGCCCTTCCCTTTGGAGATCTGCCCATGGGATACCAACATCTGCATACCCAGCTCCAG
 TATGAGTGATCTCACCTTCTACCGCGCCTGGGCAGCAGCAGGAGACATGCTGAGGACTGGGAAGTGGAG
 TGGGCGGGCACCATCTGCATCCCTATCTCGCGGAAATTTGAGAACATCACTGCTCCAAAGACCCAGGGGTTGC
 GCTGGCCGTGGCAGGCAGCTCTACAGGAGGACAGCGGGGTGCTGACGGCAGCCTACACAAGGGAGCGTGG
 TTCTAGTCTGCAGCGTGCCTGCTGATGAGCGCACTGTGGTGGTGGCTGCCCATCTGTTTACTGACCTGGG
 GAAGGTCAACATGATCAAGACAGCAGACCTGAAAGTTGTTTGGGGAATTTACCGGGATGATACCGGGATG
 AGAAGACCATCCAGAGCCTACAGATTCTGCTATCATTTGCACTCCCAACTATGACCCCATCTGCTTGTATGCT
 GACATCGCCATCCTGAAGCTCCTAGACAAGGCCCGTATCAGCACCCGAGTCCAGCCCATCTGCCCTCGCTGCCAG
 TCGGGATCTCAGCACTTCTTCCAGGAGTCCACATCACTGTGGCTGGTGGAAATGTCCTGGCAGACGCTGAGGA
 GCCCTGGCTTCAAGAAGCAGACACTGCGCTCTGGGGTGGTCACTGTGGTGGACTGCTGCTGTGTGAGGAGCAG
 CATGAGGACCATGGCATCCAGTGTGCTCACTGATAACATGTTCTGTGCCAGCTGGGAACCCACTGCCCTTCT
 TGATATCTGCACTGCAGACAGGAGGCATCGCGGCTGTGCTTCCCGGAGCAGGATCTCCTGAGCCACGCT
 GGCATCTGTGGGACTGCTCAGCTGGAGCTATGATAAAACATGCAGCCACAGGCTCTCCACTGCCCTCACCAAG
 GTGCTGCCCTTTTAAAGACTGGATTGAAAGAAATATGAAATGAACCATGCTCATGCACTCCTTGAGAAGTGTTC
 TGTATATCCGTCTGTAGCTGTGCTATTGCTGAAGCAGTGTGGGCTGAAGTGTGATTGGGCTGTGAACCTTGG
 CTGTGCCAGGGCTTCTGACTTTCAGGGACAAAATTCAGTGAAGGGTGAAGTACACTCCATTGCTGGTAGGCTGAT
 GCCGCTCCACTACTAGGACAGCCATTTGAAGATGCCAGGGCTTGAAGAAGTAAATTTCTTCAAGAAAGACC
 ATATACAAAACCTCTCACTTCCACTGACCTGGTGCTTCCCAACTTTCAGTTATACGAATGCCATGACCTTG
 ACCAGGGAAGATCTGGCTTCATGAGGCCCTTTTGGGCTCTCAAGTTCTAGAGAGCTGCTGTGGGAGAGCC
 CAGGCAAGCAGCTGGGATGTGGTGCATGCCCTTTGTGTACATGGCCAGAGTCTGTGGTCTTTTCCCTTCC
 CCATCTCTTGTACACATTTTAAATAAAATAAGGGTTGGCTTCTGAACACAAAAAATAAAAAAAAAAAAAA
 AA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 159

MELGCWTQLGLTFLQLLLLISSLPREYTVINEACPGAERNIMCRECCEYDQIECVCPGKREVV
GYTIPCCRNEENECDSCLIHPGCTIFENCKSCRNGSWGGLDDDFYVKGFYCAECRAGWYGGD
CMRCGQVLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRD
GDNRDGQIIKRVCGNERPAPIQSIGSSLHVLFHSDGSKNFDGFFHAIYEEITACSSSPCFHDG
TCVLDKAGSYKCACLAGYTGQRCENLLEERNCSDPGGFVNGYQKITGGPGLINGRHAKIGTV
VSFFCNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISDLVRRRVLPMQVQSRETPLH
QLYSAAFSKQKLSAPTCKPALPFGDLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGK
WSGRAPSCIPICGKIENITAPKTQGLRWPQAAIYRRTSGVHDGSLHKGAWFLVCSGALVNE
RTVVVAHCVTDLGKVTMIKTADLKVVLGKFYRDDDRDEKTIQSLQISAIILHPNYDPILLD
ADIAILKLLDKARISTRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTLRSG
VVSVDLSLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDICTAETGGIAAVSFPGRASPEPR
WHLMGLVSWSYDKTCSHRLSTAFTKVLPFKDWIERNMK

FIGURE 160

ACCAGGCATTGTATCTCTCAGTTGTGCATCAAGTTTCGCAATCAGATTGGAAAAAGCTCAACTCTG
 AGCTTTCTTGCCCTGCAGTGAAGCAGAGAGATAGATATTATTCACGTAATAAAAAACATGGGC
 TTCAACCTGACTTTCCACCTTTCCTACAAATTCGATTACTGTTGCTGTTGACTTTGTGCCT
 GACAGTGGTGGTGGGCGGCCACCACTACTTCTGTTGGTGCCTTCAAGAGATTCTTAAAG
 CAAAGGAGTTCATGGCTAATTTCCATAAGACCCCTCATTTTGGGGAAGGGAAAACTCTGACT
 AATGAAGCATCCACGAAGAAGGTAGAACTTGACAACTGTCCTTCTGTGTCCTTACCTCAG
 AGGCCAGAGCAAGCTCATTTTCAAACCAGATCTCACTTTGGAAGAGGTACAGGCAGAAAACT
 CCAAAGTGTCAGAGGCCCGGTATCGCCCTCAGGAATGTAAGCTTTACAGAGGGTCGCCATC
 CTCGTTCCCCACCGGAACAGAGAGAAACCTGATGTACCTGCTGGAACATCTGCATCCCTT
 CCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTCATCCACCAGGCTGAAGGTAAAAAGT
 TTAATCGAGCCAAACTCTTGAATGTGGGCTATCTAGAAGCCCTCAAGGAAGAAAAATTGGGAG
 TGCTTTATATTCCACGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTTACAAGTGTGA
 GGAGCATCCCAAGCATCTGGTGGTTGGCAGGAACAGCAGCTGGGTACAGGTTAGCTTACAGTG
 GATATTTTGGGGGTTGTTACTGCCCTAAGCAGAGACGAGCTTTTCAAGGTACATGGATTCTCT
 ACAACTACTGGGATGGGGAGGCGCAAGACGATGACCTCAGACTCAGGGTTGAGCTCCAAAG
 AATGAAAAATTTCCGGGCCCTGCCTGAAGTGGGTAAATATACAATGGTCTTCCACACTAGAG
 ACAAAAGGCAATGAGGTGAACGCAGAACGGATGAAGCTCTTACACCAAGTGTCACGAGTCTGG
 AGAACAGATGGGTTGAGTGTGTTCTTATAAATTAGTATCTGTGGAACACAATCCTTTATA
 TATCAACATCACAGTGGATTCTGGTTTGGTGCATGACCCCTGGATCTTTTGGTGATGTTTGG
 AAGAAGTGAATCTTTGTTTGCATAAATTTTGGCCTAGAGACTTCAAATAGTAGCACACATTA
 AGAACCTGTTACAGCTCATTGTTGAGCTGAATTTTTCTTTTGTATTTTCTTAGCAGAGCT
 CCTGGTGATGTAGAGTATAAAACAGTTGTAACAAGACAGCTTCTTAGTCATTTTGATCATG
 AGGGTTAAATATTGTAATATGGATACTTGAAGGACTTTATATAAAAGGATGACTCAAAGGAT
 AAAATGAACGCTATTGAGGACTCTGGTTGAAGGAGATTATTTAAATTTGAAGTAATATAT
 TATGGGATAAAAGGCCACAGGAAATAAGACTGCTGAATGCTCTGAGAGAACCAGAGTTGTTCT
 CGTCCAAGGTAGAAAAGGTACGAAGATACAATACTGTATTTCATTTATCCTGTACAATCATCT
 GTGAAGTGGTGGTGTGAGGTGAGAAGGCGTCCACAAAAGAGGGGAGAAAAGGCGACGAATCA
 GGACACAGTGAACCTGGGAATGAAGAGGTAGCAGGAGGGTGGAGTGTGCGCTGCAAGGCAG
 CAGTAGCTGAGCTGGTTGCAGGTGCTGATAGCCTTCAGGGGAGGACCTGCCAGGTATGCCT
 TCCAGTGATGCCACAGAGATAAATCTCTATTAGTTTATGTTTAAAGAGTTTTTGTAAATGA
 TTTTGTACAAGTAGGATGATGAATTAGCAGTTTACAAGTTTACATATTAACTAATAATAATA
 TGCTCATCAATACTCTGTAGTAAATGTGAAAAGGCAAAA

FIGURE 161

MGFNLT FHLSYKFRLLLLLTCLTVVGWATSNYFVGAIQEIPKAKEFMANFHKTILLGKGT
LTNEASTKKVELDNCPSVSPYLRGQSKLIFKPDLTLEEVDQAENPKVSRGRYPQECKALQRV
AILVPHRNREKHLMYLLEHLHPFLQRQQLDYGIYVIHQAEQKKFNRAKLLNVGYLEALKEEN
WDCFI FHDVDLVPENDFNLYKCEEHPKHLVVGGRNSTGYRLRYSYFGGVGTALSREQFFKVN
FSNNYWGWWGEGDDDLRLRVELQRMKISRPLPEVGKTYTMVFHTRDKGNEVNAERMKLLHQVSR
VWRTDGLSSCSYKLVSEHNPLYINITVDFWFGA

Important features:**Signal peptide:**

amino acids 1-27

N-glycosylation sites:

amino acids 4-7, 220-223 and 335-338

Xylose isomerase proteins:

amino acids 191-201

CTGGTGGCCGGGGTGCGCAGCGGGCTGTGGGCGCCCCGGAGGAGCAGCCGCCAGTTCTC
GAGCTCCAGCTGCATTCCTCCCGCTCCGCGCCACCGTTCTCCCGCTCCGGGCGCCGCA**ATG**
GCCAGGACAGTGTGGTGCGCCTCGCGCGATCTCTGGCTTGCTGCTCTGCTCCCTGCCCTGGCG
CCCCGACGAGGGGTGGCCGACGGGCTGTATGAATCAATCTCACCCAGATAGCCTCGCCACCA
CGGGAGCGGCTGGTGACCATCTCGCCAGCCTGGTGGCAAGGACAACGGCAGCTGGCCCT
CCCGCTGACGCCCACTCTACCGCTTTCATCGATGGATCCACACCCCGCTGGTGCTTACTGGCAA
GATGGAGAAGGGTCTCAGCTCCACATCCGTGTGGTGGCGACGCTGCCCGGGGAATTCCTGG
TCTGTCTGGGTCACTCCGCTGACTGCTGGATGTGCCAGCTGTGGCCAGGGGCTTGTG
GTCTTCCCATCACAGAGTTCTCTGTGGGGGACCTTGTGTGTCACCCAGAACACTTCCCTACC
TGTGGCCAGCTCTATCTACTAAGACCGTCTGAAAGTCTCTCTCTCTCCACAGCCGA
GCAACTTCTCAAGACCGCTTGTTTCTCTACAGCTGGAACTTGGGAGCGGGACGGAGTGA
GTGACTGAAGACTCCCGTGGTCTTAATAAATCTTCATCATCGGGACCTTCACCGTGAAGT
CAAGTGTGGTGGGAGTGGGAAGAGTGGAGCCGGATGCCACGAGGCTGTGAAGCAGAAGA
CCGGGGAATCTCCGCTCGCTGAAGCTGAGGAACCCCTCGAGGCATCCAAGTGTGGGG
CCCCACTTAATCAGACCTTCCAAGAAGATGACCGTACCTTGAATCTCTGGGAGGCCCTTC
TGTAGTGTGTGCTGGGCTCTCAAGCTGAGTGCTCCCGTGGAGGAAGGGAGTGGCAAC
CTGTGTCCGTGGCCAGCAGCAAGCTACAACCTTGACCCACACCTTCAGGAGCCCTGGGGACTAC
TGCTTCAGCATCCGGGCGCAGAAATATCATCAGCAAGACACATCAGGACCAAGATCCAGT
GTGGCCCTCCAGAAATCAGCCGGCTGTCTTGTCTTCCATGTGCTACACTTATCACTGTGA
TGTGGGCTTTCATCATGTATGATGACCTCCGGAATGCCATCAGCAAAAGACATGTGGGAG
AACCCGAGGCCACCTCTGGGCTGAGGTGCTGCTGCCAGATGTGCTGTGGGCTTTTGTGCT
GGAGACTCCATCTGAGTACCTGGAATTTGTTCTGTGAGAACCCAGGGCTGCTCCCGCCCTCT
ATAAGCTGTGCAAAATTCACCGCT**TCGA**CAGCACTCCCCCTCCCCACCCCTCTCAGTGTAA
CTGACTGCTGACTTGGAGTTTCCAGCGAGGCTGGTGTGCACCACTGACCAAGGAGGGTTCATT
TGGCTGTGGGCTGTGGCGCTGGATCATCCATCCATCTGTACAGTTTCAGCAGTGTCCACAAAGC
CTCCCTCTCTGTACCCCTGACCCAGCCATTCACCACTCTGTACAGCTCCAGCCACTGACA
TAAGCCCCACTCGGTACACACCCCTTGACCCCTACCTTTGAAGAGGCTTCGTGCAGGACT
TTGATGCTTGGGCTGTTCCGCTGTGACTCTCATGTGGGCTGGCTGCCACTGCCCATGCCATTCCT
CTCATATTGGCAGATCTGCTGTCCATTGGGGGTTCTCAGTTTCTCCCCAGACAGCCCTTGA
CTGTGCCAGAGAGCTAGAAGAAGGTCTAAAGGGTTAAAAATCCATAACTAAAGATTGTATC
ACATAGATGGGCACTCACAGAGAGAAGTGTGCATGTACACACACACACACACACACACA
CACACACACAGAAATATAAACACTGCTGCATGACATGGGCATTCAGATGATCACTGTGTA
TCTGGTTAAGTCGGTGTCTGGATGACCCCTGCATAGAGCTGAAAGGAAATTTGACCTCCA
AGCAGCCCTGACAGGTTCTGGGCGCCGGCCCTCCCTTTGTGCTTTGTCTGCAAGTCTCTTGG
GCCCTTTATAAGGCCATCCTAGTCCCTGCTGGCTGGCAGGGGGCTGGATGGGGGGCAGGACT
AATACTGAGTGTGTCAGAGTGTCTTTATAAATACACCTATTTTATCGAAACCCATCTGTG
AAACTTCTCACTGAGGAAGAAGGCTTCGACGGGTAGAAGAGTTGAGTCAAGCGCGGGCGGCG
TGGCTCAGCCCTGTAAATCCGACACTTTTGAAGCCCGGAGCGGGTGGATCAGGAGATCAGGA
GATCGAGACCACTGCTGCTAACCGTGTGAAGCCCGCTCTACTATAAAAAATCAAAAAGTT
AGCCGGGCTGGTGGTGGGTGCTGTAGTCCAGCACTCTCGGAGGCTGAGGCAGGAGAAATG
GTGCAAGCCGGGAGCGCGAGCTTGAGTGAAGCCAGATGGCGCCACTGCATCTCAGCCTGA
GTGACAGCGCGAGCTCTGTCTCCA

FIGURE 163

MAQAVWSRLGRILWLACLLPWAPAGVAAGLYELNLTTDSPATTGAVVTISASLVAKDNGSLA
LPADAHLYRFHWIHTPLVLTGKMEKGLSSTIRVVGHVPGEFPVSVVWTAADCWMCQPVARGF
VVLPITEFLVGDVVTQNTSLPWPSSYLTKTVLKVSFLLHDP SNFLKTALFLYSWDFGDGTQ
MVTEDSVVYNYNSIIIGTFTVKLKVVAEWEEVEPDATRAVKQKTGDFSASLKLQETLRGIQVL
GPTLIQTFQKMTVTNLNFGSPPLTVCWRLKPECLPLEEGECHPVSVASTAYNLTHTRDPGD
YCF SIRAENIISKTHQYHKIQVWPSRIQPAVFAFP CATLITVMLAFIMYMTLRNATQQKDMV
ENPEPPSGVRCCCMCCGPFLETPSEYLEIVRENHGLLPPLYKSVKTYTV

Important features of the protein:**Signal peptide:**

amino acids 1-24

Transmembrane domain:

amino acids 339-362

N-glycosylation sites.

amino acids 34-37, 58-61, 142-145, 197-200, 300-303 and 364-367

[illegible]

FIGURE 165

MALSSQIWAACLLLLLLASLTSGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRRDTH
FPICIFCCGCCHRSKCGMCKCT

FIGURE 166

CTGT CAGGAAGGACCATCTGAAGGCTGCAATTTGTTCTTAGGGAGGCAGGTGCTGGCCCTGGC
 CTGGATCTTCCACC**ATG**TTCTCTGTGCTGCTTTTGATAGCCTGATTGTCAACCTTCTGGGC
 ATCTCCCTGACTGTCTCTTCCACCTCCTTCTCGTTTTCATCATAGTGCCAGCCATTTTGG
 AGTCTCCTTTGGTATCCGCAAACTCTACATGAAAAGTCTGTTAAAAATCTTTGCGTGGGCTA
 CCTTGAGAATGGAGCGAGGAGCCAAGGAGAAGAACCACAGCTTTACAGCCCTACACCAAC
 GGAATCATTGCAAGGATCCCACTTCACTAGAAGAAGAGATCAAGAGATTTCGTGGAAGTGG
 TAGTAGTAAGGCTCTGGACAACACTCCAGAGTTCGAGCTCTCTGACATTTTCTACTTTTGCC
 GGAAGGATGGAGACCATTATGGATGATGAGGTGACAAAGAGATTCTCAGCAGAAGAACTG
 GAGTCTCTGGAACCTGCTGAGCAGAACCAATTATAACTTCCAGTACATCAGCCTTCGGCTCAC
 GGTCTGTGGGGTTAGGAGTGTGATTTCGGTACTGCTTTCTGCTGCCGCTCAGGATAGCAC
 TGGCTTTCACAGGGATTAGCCTTCTGGTGGTGGGCACAACCTGTGGTGGGATACTTGCCAAAT
 GGGAGGTTTAAGGAATTCATGAGTAAACATGTTCACTTAATGTGTTACCGGATCTCGGTGCG
 AGCGCTGACAGCCATCATCACCTACCATGACAGGGAAAACAGACCAAGAAATGGTGGCATCT
 GTGTGGCCAATCATACCTCACCGATCGATGTGATCATCTTGGCCAGCGATGGCTATTATGCC
 ATGGTGGGTCAAGTGCACGGGGGACTCATGGGTGTGATTACAGAGACCATGGTGAAGCCCTG
 CCCACACGTCTGGTTTGAGCGCTCGGAAGTGAAGGATCGCCACCTGGTGGCTAAGAGACTGA
 CTGAACATGTGCAAGATAAAAGCAAGCTGCCTATCCTCATCTTCCAGAAGGAACCTGCATC
 AATAATACATCGGTGATGATGTTCAAAAAGGGAAGTTTTGAAATTGGAGCCACAGTTTACCC
 TGTGCTATCAAGTATGACCCCAATTTGGCGATGCCTTCTGGAACAGCAGCAAAATACGGGA
 TGGTGACGTACCTGCTGCGAATGATGACCAGCTGGGCCATTGTCTGCAGCGTGTGGTACCTG
 CCTCCCATGACTAGAGAGGCAGATGAAGATGCTGTCCAGTTTGGGAATAGGGTGAATCTGC
 CATTGCCAGGCAGGGAGGACTTGTGGACCTGCTGTGGGATGGGGGCCCTGAAGAGGGAGAAGG
 TGAAGGACACGTTCAAGGAGGAGCAGCAGAAGCTGTACAGCAAGATGATCGTGGGGAACCCAC
 AAGGACAGGAGCCGCTCT**GAG**ACCTGCCCTCCAGCTGGCTGGGGCCACCGTGCGGGGTGCCAA
 CGGGCTCAGAGCTGGAGTTGCCGCCGCCCCCACTGCTGTGTCCTTCCAGACTCCAGGG
 CTCCCCGGGTGCTCTGGATCCCAGGACTCCGGCTTTCGCCGAGCCGACGCGGATCCCTGT
 GCACCCGGCGCAGCCTACCCTTGGTGGTCTAAACGGATGCTGCTGGGTGTTGCGACCCAGGA
 CGAGATGCCTTGTTCTTTTACAATAAGTCTGTGGAGGAATGCCATTAAAGTGAACCTCCCA
 CCTTTGCACGCTGTGCGGGCTGAGTGGTGGGGAGATGTGCCATGGCTTTGTGCTAGAGAT
 GGCGGTACAAGAGTCTGTTATGCAAGCCCGTGTGCCAGGATGTGCTGGGGGCGGCCACCCG
 CTCTCCAGGAAAGGCACAGCTGAGGCACCTGTGGCTGGCTTCGGCCTCAACATCGCCCCAGC
 CTTGGAGCTCTGCAGACATGATAGGAAGGAACTGTCATCTGCAGGGGCTTTTCAGCAAAATG
 AAGGGTTAGATTTTATGCTGCTGCTGATGGGGTTACTAAAGGAGGGGAAGAGGGCGAGTG
 GGCGCTGACTTGGGCCATGGGGAGAACGTGTGTTCTGTACTCCAGGCTAACCTGAACCTCCC
 ATGTGATGCGCGCTTTGTTGAATGTGTCTCGGTTTCCCATCTGTAATATGAGTCGGGGG
 GAATGGTGGTGAATCTTCACTCAGGGCTGTTGTGGGATTAAGTGTCTGCGGGTGAGTGA
 AGGACATCACGTTCACTGTTTCAAGTACAGGCCACAAACGGGGCACGGCAGGCCTGAG
 CTCAGAGCTGCTGCATGGGCTTTGGATTGTTCTTGTGAGTAAATAAACTGGCTGGTGAA
 TGA

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FIGURE 167

MFLLLPFDSLIVNLLGISLTVLFTLLLVFIIVPAIFGVSFQIRKLYMKSLLKIFAWATLRME
RGAKENHQLYKPYTNGIIAKDPTSLEEEIKEIRRSKSSKALDNTPEFELSDIFYFCRKGME
TIMDDEVTKRFSAEELSWNLLSRTNYNFQYISLRLTVLWGLGVLIRYCFLLPLRIALFTG
ISLLVVGTTVVGYPNGRFKEFMSKHVHLMCYRICVRALTAITYHDRENRPNGGICVANH
TSPIDVILASDGYAMVGQVHGGLMGVIQRAMVKACPHVWFERSEVKDRHLVAKRLTEHVQ
DKSKLPILIFPEGTCINNTSVMFKKGSFEIGATVYPVAIKYDPQFGDAFWNSSKYGMVTYL
LRMTSWAIVCSVWYLPMTREADEDAVQFANRVKSAIARQGGLVDLLWDGGLKREKVKDTF
KEEQQLYSKMIVGNHKDRSRS

FIGURE 168

GCCCCCTCGAAACCAGGACTCCAGCACCTCTGGTCCC GCCCTCACCCGGACCCCTGGCCCTCA
 CGTCTCCTCCAGGGAATGGCGCTGGCGGCTTTGATGATCGCCCTCGGCAGCCTCGGCCTCCAC
 ACCTGGCAGGCCAGGCTGTTCCCAACCATCCTGCCCTGGGCCTGGCTCCAGACACCTTTGA
 CGATACCTATGTGGGTTGTGCAGAGGAGATGGAGGAGAAGGCAGCCCCCTGCTAAAGGAGG
 AAATGGCCCAACCATGCCCTGCTGCGGGAATCCTGGGAGGCAGCCAGGAGACCTGGGAGGAC
 AAGCGTCGAGGGCTTACCTTGCCCCCTGGCTTCAAAGCCCAGAATGGAATAGCCATTATGGT
 CTACACCAACTCATCGAACACCTTGTA CTGGGAGTTGAATCAGGCCGTGCGGACGGGCGGAG
 GCTCCCGGAGCTCTACATGAGGCACCTTTCCCTTCAAGGCCCTGCATTTCTACCTGATCCGG
 GCCCTGCAGCTGCTGCGAGGCAGTGGGGCTGCAGCAGGGGACCTGGGGAGGTGGTGTTCCG
 AGGTGTGGGCAGCCTTCGCTTTGAACCCAAGAGGCTGGGGGACTCTGTCCGCTTGGGCCAGT
 TTGCCTCCAGCTCCCTGGATAAGGCAGTGGCCACAGATTGGGGAGAAGAGGCGGGGCTGT
 GTGTCTGCGCCAGGGGTGCAGCTAGGGTCACAATCTGAGGGGGCTCCTCTGCCCCCTG
 GAAGACTCTGCTCTTGCCCCCTGGAGAGTTCCAGCTCTCAGGGGTTGGGCCCTGAAGTCCA
 ACATCTGCCACTTAGGAGCCCTGGGAACGGGTGACCTTCATATGACGAAGAGGCACCTCCAG
 CAGCCTTGAGAAGCAAGAACATGGTTCGGGACCCAGCCCTAGCAGCCTTCTCCCCAACCAGG
 ATGTTGGCCTGGGGAGGCCACAGCAGGGCTGAGGGAACCTGCTATGTGATGGGGACTTCCT
 GGGACAAGCAAGGAAAGTACTGAGGCAGCCACTTGATTGAACGGTGTGCAATGTGGAGACA
 TGGAGTTTATTGAGGTAGCTACGTGATTAAATGGTATTGCAGTGTGGA

FIGURE 169

MALAALMIALGSLGLHTWQAQAVPTILPLGLAPDTFDDTYVGC AEEMEEKAAPLLKEEMAHH
ALLRESWEAAQETWEDKRRGLTLP PGFKAQNGIAIMVYTNSNTLYWELNQAVRTGGGSREL
YMRHFPPKALHFYLI RALQLLRGSGGCSRGPGEVVFRGVGSLRFEPKRLGDSVRLGQFASSS
LDKAVAHRFGEKRRGCVSAPGVQLGSQSEGASSLPPWKTLL LAPGEFQLSGVGP

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GTGGCTTCATTTTCAGTGGCTGACTTCCAGAGAGCAATATGGCTGGTTCCTCCCAACATGCCTCA
CCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAAGAGCTG
GTCGGTTCGGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTCCAAAGTAAAGCAAGTTGACTC
TATTGTCTGGACCTTCAACACAACCCCTCTGTGCACCATACAGCCAGAAGGGGGCACTATCA
TAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCAGATGGAGGCTACTCCCTGAAG
CTCAGCAAACCTGAAGAAGATGACTCAGGATCTACTATGTGGGGATATACAGCTCATCACT
CCAGCAGCCCTCCACCAGGAGTACGTGCTGCATGTCTACGAGCACTGTCAAAGCCTAAAG
TCACCATGGGTCTGCAGAGCAATAAGAATGGCACTGTGTGACCAATCTGACATGCTGCATG
GAACATGGGGAGAGGATGTGATTTATACCTGGAAGGCCCTGGGGCAAGCAGCCAATGAGTC
CCATAATGGGTCCATCCTCCCATCTCCTGGAGATGGGGAGAAAAGTGATATGACCTTCATCT
GCGTTGCCAGGAACCCTGTCAGCAGAAACCTCTCAAGCCCCATCCTTGCCAGGAAGCTCTGT
GAAGGTGCTGCTGATGACCCAGATTCTCCATGGTCTCCTGTGCTCCTGTGGTGCCCT
CCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTGGTTTCTGAAGAGAGAGACAGAAG
AGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTGGGAACTCTCAACATATGCCCCAT
TCTGGAGAGAACACAGAGTACGACACAATCCCTCACATAATAGAACCAATCTTAAGGAAGA
TCCAGCAAATACGGTTTACTCCACTGTGGAAATACCGAAAAAGATGGAATATCCCACTCAC
TGCTCAGATGCAGACACACCAAGGCTATTGTACCTATGAGAATGTTATCTAGACAGCAGTG
CACTCCCCTAAGTCTCTGCTCA

FIGURE 171

MAGSPTCLTLIYLWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPLVT
IQPEGGTIIVTQNRNRERVDFFDGGYSLKLSKLKNDSGIYYVGIYSSSLQQPSTQEYVLHV
YEHLSKPKVTMGLQSNKNGTCVTNLTCMEHGEEVDIYTWKALGQAANESHNGSILPISWRW
GESDMTFICVARNPVSRNFSSPILARKLCBGAADDPDSSMVLLCLLLVPLLLSLFVLGLFLW
FLKRERQEEYIEEKRVDICRETPNICPHSGENTYDTIPHTNRTILKEDPANTVYSTVEIP
KKMENPHSLLTMPDTPRLFAYENVI

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FIGURE 172

CTGGTTCCCCAACATGCCTCACCCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCC
TCTGGACCCGTGAAAGAGCTGGTCGGTTCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTC
CAAAGTAAAGCAAGTTGACTCTATTGTCTGGACCTTCAACACAACCCCTCTTGTCAACCATAC
AGCCAGAAGGGGGCACTATCATAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCA
GATGGAGGCTACTCCCTGAAGCTCAGCAAACCTGAAGAAGAATGACTCAGGGATCTACTATGT
GGGGATATACAGCTCATCACTCCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACG
AGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTG
ACCAATCTGACATGCTGCATGGAACATGGGGAAGAGGATGTGATTATACCTGGAAGGCCCT
GGGGCAAGCAGCCAATGAGTCCCATATGGGTCCATCCTCCCCATCTCCTGGAGATGGGGAG
AAAGTGATATGACCTTCATCTGCGTTGCCAGGAACCCCTGTCAGCAGAAAACCTCTCAAGCCCC
ATCCTTGCCAGGAAGCTCTGTGAAGTGCTGCTGATGACCCAGATTCTCCATGGTCCTCCT
GTGTCTCCTGTTGGTGCCCCCTCCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTGGTTTC
TGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTCGGGAA
ACTCCTAACATATGCCCCATTCTGGAGAGAAACAGAGTACGACACAATCCCTCACACTAA
TAGAACAAATCCTAAAGGAAGATCCAGCAAATACGGTTTACTCCACTGTGGAATACCGAAAA
AGATGGAAAATCCCCTCACTGCTCAGATGCCAGACACCAAGGCTATTTGCCTATGAG
AATGTTATCTAGACAGCAGTGCACTCCCCTAAGTCTCTGCTCAAAAAAAAAAAAAAAAAA

FIGURE 173

GAAAGACGTGGTCTCTGACAGACAGACAATCCTATTCCCTACCAAAATGAAGATGCTGCTGCT
GCTGTGTTTGGGACTGACCCTAGTCTGTGTCCATGCAGAAGAAGCTAGTTCTACGGGAAGGA
ACTTTAATGTAGAAAAGATTAATGGGGAATGGCATACTATTATCCTGGCCTCTGACAAAAGA
GAAAAGATAGAAGAACATGGCAACTTTAGACTTTTTCTGGAGCAAATCCATGTCTTGGAGAA
TTCCTTAGTTCTTAAAGTCCATACTGTAAGAGATGAAGAGTGCTCCGAATTATCTATGGTTG
CTGACAAAACAGAAAAGGCTGGTGAATATTCTGTGACGTATGATGGATTCAATACATTTACT
ATACCTAAGACAGACTATGATAACTTTCTTATGGCTCACCTCATTAACGAAAAGGATGGGGA
AACCTTCCAGCTGATGGGGCTCTATGGCCGAGAACCAGATTTGAGTTCAGACATCAAGGAAA
GGTTTGCACAACATATGTGAGGAGCATGGAATCCTTAGAGAAAATATCATTGACCTATCCAAT
GCCAATCGTGCCCTCCAGGCCCGAGAATGAAGAATGGCCTGAGCCTCCAGTGTTGAGTGGAC
ACTTCTCACCAGGACTCCACCATCATCCCTTCTTATCCATACAGCATCCCCAGTATAAATTC
TGTGATCTGCATTCCATCCTGTCTCACTGAGAAGTCCAATTCCAGTCTATCAACATGTTACC
TAGGATACCTCATCAAGAATCAAAGACTTCTTTAAATTTCTCTTTGATACACCCCTTGACAAAT
TTTTCATGAATATTCTCTCTCTGTTCAATAAATGATTACCCTTGCACTTAA

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FIGURE 174

MKMLLLCLGLTLVCVHAEASSTGRNFNVEKINGEWHTIILASDKREKIEEHGNFRLFLEQ
IHVLENSLVLVKVHTVRDEECSELSMVADKTEKAGEYSVTYDGFNTFTIPKTDYDNFLMAHLI
NEKDGETFQLMGLYGREPDLSSDIKERFAQLCEEHGILRENIIDLSNANRCLQARE

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FIGURE 175

GGCTCGAGCGTTTCTGAGCCAGGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGCAA
TGGATTTCAGCCTGCTGGTTCTACTGCTGTAGGAGTAGTTCTCAATGCGATACCTCTAATTG
TCAGCTTAGTTGAGGAAGACCAATTTTCTCAAAACCCCATCTCTTGCTTTGAGTGGTGGTTC
CCAGGAATTATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACAATGTCCTTGACAGCAAG
AAAAAGAGCGTGCTGCAACAACAGAACTGGAATGTTTCTTTCATCATTTTTCAGTGTGATCA
CAGTCATTGGTGCTCTGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAGGTCCTCTC
ATGTGTAATTCTCCAAGCAACAGTAATGCCAATTGTGAATTTTCATTGAAAAACATCAGTGA
CATTTCATCCAGAATCCTTCAACTTGCAGTGGTTTTTCAATGACTCTTGTGCACCTCCTACTG
GTTTCAATAAAACCCACCAGTAACGACACCATGGCGAGTGGCTGGAGAGCATCTAGTTTCCAC
TTCGATTCTGAAGAAAACAAACATAGGCTTATCCACTTCTCAGTATTTTAGGTCTATTGCT
TGTGTTGAATTCTGGAGGTCTCTTTGGGCTCAGTCAGATAGTCATCGGTTTCTTGGCTGTC
TGTGTGGAGTCTCTAAGCGAAGAAGTCAAATTGTGTAGTTTAATGGGAATAAAATGTAAGTA
TCAGTAGTTTGAAAAAAAAA

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FIGURE 176

MTCCEGWTSCNGFSLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMA
IPATTMSLTARKRACCNRTGMFLSSFFSVITVIGALYCM LISIQALLKGPLMCN SPSNSNA
NCEFS LKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDT MASGWRASSFHF DSEENKHRL
IHFSVFLG LLLVGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV

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TOTAL: 0440660

FIGURE 177

GTTCGAATCCAAATCACTCATTGTGAAAGCTGAGCTCACAGCCGAATAAGCCACC**ATG**AGGCT
GTCAGTGTGTCTCCTGATGGTCTCGCTGGCCCTTTGTGCTACCAAGGCCCATGCTCTTGTCT
GCCCAGCTGTTGCTTCTGAGATCACAGTCTTCTTATTCTTAAGTGACGCTGCGGTAAACCTC
CAAGTTGCCAAACTTAATCCACCTCCAGAAGCTCTTGACCCAAGTTGGAAGTGAAGCACTG
CACC GATCAGATATCTTTTAAAGAAACGACTCTCATTGAAAAAGTCTCTGGTGAAA**TAG**TGAA
AAAATGTGGTGTGTGACATGTAAAAATGCTCAACCTGGTTTCCAAGTCTTTCAACGACACC
CTGATCTTCACTAAAAATGTAAAGTTTCAACACGTGTGCTTTAATAAATCACTTGCCCTGC

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FIGURE 178

MRLSVCLLMVSLALCCYQAHALVCPAVASEITVFLFLSDAAVNLQVAKLNPPPEALAAKLEV
KHCTDQISFKKRLSLKKSWWK

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FIGURE 179

ATCCGTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTCGCCAAGGTGACCTCGCAGGACACTGG
TGAAGGAGCAGTGAGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTG
GAGCAGATCCGTGGGCTGCAGACCCCGCCCCAGTGCCCTCTCCCCTGCAGCCCTGCCCCTC
GAACTGTGACATGGAGAGAGTGACCCTGGCCCTTCTCCTACTGGCAGGCCTGACTGCCTTGG
AAGCCAATGACCCATTTGCCAATAAAGACGATCCCTTCTACTATGACTGGAAAAACCTGCAG
CTGAGCGGACTGATCTGCGGAGGGCTCCTGGCCATTGCTGGGATCGCGGCAGTTCTGAGTGG
CAAATGCAAATACAAGAGCAGCCAGAAGCAGCACAGTCCTGTACCTGAGAAGGCCATCCCAC
TCATCACTCCAGGCTCTGCCACTACTTGCTTGAGCACAGGACTGGCCTCCAGGGATGGCCTGA
AGCCTAACACTGGCCCCAGCACCTCCTCCCCTGGGAGGCCTTATCCTCAAGGAAGGACTTC
TCTCCAAGGGCAGGCTGTTAGGCCCTTTCTGATCAGGAGGCTTCTTTATGAATTAACTCG
CCCCACCACCCCTCA

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FIGURE 180

MERVTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAAGIAAVLSGKCK
YKSSQKQHSPVPEKAIPILITPGSATTC

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FIGURE 181

GGAGAAGAGGTTGTGTGGGACAAGCTGCTCCCGACAGAAGG**ATG**TCGCTGCTGAGCCGTGCC
 TGGCTGGGCCTCAGACCGGTGGCAATGTCCCATGGCTACTCCTGCTGCTGGTTGTGGGCTC
 CTGGCTACTCGCCCGCATCCTGGCTTGGACCTATGCCTTCTATAACAAGTCCGCGCGGCTCC
 AGTGTTTTCCACAGCCCCAAAACGGAAC**TGG**TTTTGGGGTCACCTGGGCCTGATCACTCCT
 ACAGAGGAGGGCTTGAAGGACTCGACCCAGATGTCGGCCACCTATTCCAGGGCTTTACGGT
 ATGGCTGGGTCCCATCATCCCTTCATCGTTTTATGCCACCTGACACCATCCGGTCTATCA
 CCAATGCCTCAGCTGCCATTGCACCCAAGGATAATCTCTTCATCAGGTTCTGAAGCCCTGG
 CTGGGAGAAGGGATACTGCTGAGTGGCGGTGACAAGTGGAGCCGCCACCGTCGGATGCTGAC
 GCGCGCCTTCCATTTCAACATCCTGAAGTCTATATAACGATCTTCAACAAGAGTGCAAACA
 TCATGCTTGACAAGTGGCAGCACCTGGCCTCAGAGGGCAGCAGTCGTCTGGACATGTTTGAG
 CACATCAGCCTCATGACCTTGGACAGTCTACAGAAATGCATCTTCAGCTTTGACAGCCATTG
 TCAGGAGAGGCCCAGTGAATATATTGCCACCATCTTGGAGCTCAGTGCCCTTGTAGAGAAAA
 GAAGCCAGCATATCTCCAGCACATGGACTTTCTGTATTACCTCTCCCATGACGGGCGGCGC
 TTCCACAGGGCCTGCCGCTGGTGCATGACTTCACAGACGCTGTCTATCCGGGAGCGCGCTCG
 CACCTCCCCACTCAGGGTATTGATGATTTTTTCAAAGACAAAGCCAAGTCCAAGACTTTGG
 ATTTTCATGTATGTCTTCTGCTGAGCAAGGATGAAGATGGGAAGGCATTGTCAGATGAGGAT
 ATAAGAGCAGAGGCTGACACCTTCATGTTTGGAGGCCATGACACCACGGCCAGTGGCCTCTC
 CTGGGTCTGTACAACCTTGCAGGACCCAGAATACCAGGAGCGCTGCCGACAGGAGGTGC
 AAGAGCTTCTGAAGGACCGCATCCTAAAGAGATTGAATGGGACGACCTGGCCCAGCTGCC
 TTCTGTACCATGTGCGTGAAGGAGAGCCTGAGGTTACATCCCCAGCTCCCTTCATCTCCCG
 ATGCTGCACCCAGGACATTGTTCTCCAGATGGCCGAGTCATCCCCAAAGGCATTACCTGCC
 TCATCGATATTATAGGGTCCATCACAACCCAACTGTGTGGCCGGATCCTGAGGTCTACGAC
 CCCTTCCGCTTTGACCCAGAGAAACAGCAAGGGGAGGTCACTCTGGCTTTTATTCCTTTCTC
 CGCAGGGCCAGGAACTGCATCGGGCAGGCGTTCCCATGGCGGAGATGAAAGTGGTCTTGG
 CGTTGATGCTGCTGCACTTCCGGTTCCTGCCAGACCACACTGAGCCCCGAGGAAGCTGGAA
 TTGATCATGCGCGCCGAGGGCGGGCTTTGGCTGCGGGTGGAGCCCTGAATGTAGGCTTGCA
GTGACTTTCTGACCCATCCACCTGTTTTTTTGCAGATTGTCTATGAATAAAAGGCTGCTGTCAA

MSLLSLPWLGLRPVAMSPWLLLLLVGSGWLLARILAWTYAFYNNCRRLQCFQPQPKRNWFVG
HLGLITPTEEGLKDSQMSATYSQGFTVWLGP IIPFIVLCHPDTIR SITNASAAIAPKDNLF
IRFLKPWLGE GILLSGGDKWSRHRMLTPAFHFNILKSYITIFNKSANIML DKWQHLSAEGS
SRLDMFEHISLMTLDSLQKCIFSFDSHCQERPSEYIATILELSALVEKRSQHILQHMDFLYY
LSHDGRRFRHRACRLVHDFTDAVIRERRRTLPTQGIDDFKDKAKSKTLDFIDVLLLSKDEDG
KALSDEDIRAEADTFMFGGHDTTASGLSWVLYNLARHPEYQERCRQEVQELLKDRDPKEIEW
DDLAQLPFLTMCVKESLRHPPAFIFSRCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVW
DPDEVYDPRFDPENSKRSRGLAFIPISGAFNRNIGQAFAMAEMKVVLAMLLHFRFLPDHT
EPRRKLEIMRAEAGLWL RVEPLNVGLO

FIGURE 183

CAACAGAAGCCAAGAAGGAAGCCGTCCTATCTTGTGGCGATC**ATG**TATAAGCTGGCCTCCTGC
TGTTTGCTTTTCACAGGATTCTTAAATCCTCTCTTATCTCTCCTCCTTGACTCCAGGGA
AATATCCTTTCAACTCTCAGCACCTCATGAAGACGCGCGCTTAACCTCCGAGGAGCTAGAAA
GAGCTTCCCTTCTACAGATATTGCCAGAGATGCTGGGTGCAGAAAGAGGGGATATTCTCAGG
AAAGCAGACTCAAGTACCAACATTTTAAACCAAGAGGAAATTTGAGAAAGTTTCAGGATTT
CTCTGGACAAGATCCTAACATTTTACTGAGTCATCTTTTGGCCAGAATCTGGAAACCATACA
AGAAACGTGAGACTCCTGATTGCTTCTGGAAATACTGTGTCT**TGA**AGTGAAATAAGCATCTGT
TAGTCAGCTCAGAAACACCCATCTTAGAATATGAAAAATAACACAATGCTTGATTGAAAC
AGTGTGGAGAAAACTAGGCAAACTACACCCTGTTTCATTGTTACCTGAAAAATAATCCTCT
ATGTTTTGCACAAAAAAAAAAAAAA

GAACATTTTGTAGTCCCAAGGAATGTACATCAGCCCCACGGAAGCTAGGCCACCTCTGGGAT
GGGGTTGCTGGTTTAAAACAAACGCCAGTCATCTATATAAGGACCTGACAGCCACCAGGCA
CCACCTCCGCCAGGAAGTGCAGGCCACCTGTCTGCAACCCAGCTGAGGCCATGCCCTCCCC
AGGGACCGTCTGCAGCCTCTCTCTCTCGGCATGCTCTGGCTGGACTTGGCCATGGCAGGCT
CCAGCTTCTTGAGCCCTGAACACCAGAGAGTCCAGCAGAGAAAGGAGTCGAAGAAGCCACCA
GCCAAGCTGCAGCCCCGAGCTCTAGCAGGCTGGCTCCGCCCGGAAGATGGAGGTCAAGCAGA
AGGGGCAGAGGATGAACTGGAAGTCCGGTTCAACGCCCCCTTTGATGTTGGAATCAAGCTGT
CAGGGGTTTCAGTACCAGCAGCACAGCCAGGCCCTGGGGAAAGTTTCTTCAGGACATCCTCTGG
GAAGAGGCCAAAGAGGCCCCCAAGCAGCAAGTGTCGCCCAAGCCTTACTCACCTCTCTCT
AAGTTTAGAAGCGCTCATCTGGCTTTTCTGTTCTGCTTCGAGCAACTCCCACGACTGTTGTA
CAAGCTCAGAGGCGCAATAAATGTTCAAACCTGTA

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FIGURE 186

MPSPGTVCLLLLGMLWLDLAMAGSSFLSFEHQRVQQRKESKKPPAKLQPRALAGWLRPEDG
GQAEGAEDLEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADKO

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FIGURE 187

CGGCCACAGCTGGCATGCTCTGCCTGATCGCCATCCTGCTGTATGTCTCGTCCAGTACCTC
 GTGAACCCCGGGGTGCTCCGCACGGACCCAGATGTCAAGAAT**ATGA**ACACGTGGTGCTGT
 TCCTCCCCCTGTTCCCGGTGCAGGTGCAGACCCGTAGTCTGTATCATCGGGATGCTCGTG
 CTCTGCTGGACTTTCTTGGCTTGGTGCACCTGGGCCAGCTGCTCATCTTCCACATCTACCT
 GAGTATGTCCCCACCCTAAGCCCCGATCCCCCAAGGCTGGGTGGTCAGAGCTGCTCATC
 TTACACCTCTACTTGAGTATGTCCCTAACCTGAGCCCCCACGCTGGGGCCAGAGTCTTT
 GTCCCCCGTGTGCGCATGTGTTCAAGGTGAGCTCTCCAGAAGTGAGATCATGGACAAAAA
 GGGCAATCACAGGAAGAAATTAATCCATGAGGACCCAGCAGGCCCAGCAAGAAGCTGAAC
 TCACGCCGAGACCTGCAGGAGTGGTGCCAGGTGCT**TGA**AGTAACAAGTTTAAATGTTTCA
 GACAATGGAATGGAATCTATTAGGCAAGAACAGGACATTATGAAATAAGGACAGGTGGACTT
 CCAAAAAACACAAGTAGAAATTTAACAATGAAATATATTACAGGCAGGTACCCACTAACCA
 AACAACCTGAAGCGAGAGCTGTGGTCTTGCTTGGTCTCACAGTGGGCACAGCGGTAGGCGGT
 AGTCATGTTGCTGAACGACGGAGGGTAAACTCCCCAGCCCCAAGAAAACCTGTGTTGGAAGT
 AACAACAACCTCCCTGCTCCTGGCACCAGCCGTTTTGGTTCATGGTGGGCCAGCTGCAAAGCG
 TCTTCCATTCTCTGGGCAGTGGTGGCCCCGAGGCTGTGGCCTCTCAGGGGGTTTCTGTGGAC
 ACGGGCAGCAGAGTGTGTCCAGGCCAGCCCCAAGAATGCCCTGCTCCTGACAGCTTGGCCA
 ACCCTGGTCAGGGCAGAGGGAGTTGGGTGGGTGAGGCTCTGGGCTCACCTCCATCTCCAGA
 GCATCCCCTGCCTGCAGTTGTGGCAAGAACGCCAGCTCAGAATGAACACACCCACCAAGA
 GCCTCCTGTGTCATAACCCACAGGTTACCCCTACAAACCACTGTCCCCACACAACCTGGGGAT
 GTTTTAAACACACACCTCTAACGCATATCTTACAGTCACTGTTGTCTTGCCTGAGGGTTGA
 ATTTTTTTTAAATGAAAGTGCAATGAAATCACTGGATTAAATCCTACGGACACAGAGCTGAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

MNTWLLFLFLPFPVQVQTLIVVIIIGMLVLLLDLFLGLVHLGQLLI FHIYLSMSP TSLSPRSPQGW
VVRAAHLTPLLEYVPNPEPPTPGARVFPVPRVMCSGSASPRSEIMDKKGSQEEIKSMRTQQ
AQQEAELTPRPAGVVPGA

FIGURE 189

GGAGTGCAGATGGCATCCTTCGGTTCTTCCAGACAAGCTGCAAGACGCTGACC**ATG**GCCAAAC
ATGGAGCTCTCGAAGGCCCTTCTTGGCCAGCGGACACTCCTATCTGCCATCCTCAGCATGCT
ATCACTCAGCTTCTCCACAACATCCTGCTCAGCAACTACTGGTTTGTGGGCACACAGAAG
TGCCCAAGCCCTGTGCGAGAAAAGGTCTGGCAGCCAAGTGCTTTGACATGCCAGTGTCCCTG
GATGGAGATACCAACACATCCACCAGGAGGTGGTACAATACTGGGAGACTGGGGATG
CCGTTTCTCCTCCGGAGCTTCCGGAGTGGCATGTGGCTATCCTGTGAGGAACTGTGGAAG
AACCAGGGGAGAGGTGCCGAAGTTTCATTGAACCTACACCACAGCCAAGAGAGGTGAGAAA
GGACTACTGGAATTTGCCACGTTGCAAGGCCATGTCACCCCACTCTCCGATTTGGAGGGAA
GCGGTTGATGGAGAAGGCTTCCCTCCCTCCCTTCCCTTGGGGCTTTGTGGCAAAAATCCTA
TGGTTATCCTCGGGAACGCAGATCACCTACATCGGACTTCAATTATCAGCTTCCCTCTGCT
ACTAACAGACTTGCTACTCACTGGGAACCTGCTGTGGGCTCAAATCGAGCGCCTTTGCTG
CTGTTTCTCTGTCTGTGAGGTCTCCTGGGGATGGTGGCCACATGATGTATTACAAGTC
TTCCAAGCGACTGTCAACTTGGGTCCAGAAGACTGGAGACCACATGTTTGGAAATTATGGCTG
GGCCTTCTACATGGCCTGGCTCTCCTTCACTGCTGCATGGCGTGGCTGTCACCACCTTCA
ACAGTACACCAGGATGGTGTGAGGTTCAAGTGCAAGCA**TAG**TAAAGAGCTTCAAGGAAAAC
CCGAAGTGCCTACCACATCACCATCAGTGTTTCCCTCGGCGGCTGTCAAGTGCAGCCCCAC
CGTGGGTCTTTGACCAGCTACCACCAGTATCATAATCAGCCCATCCACTCTGTCTCTGAGG
GAGTCGACTTCTACTCCGAGCTGCGGAACAAGGGATTTCAAAGAGGGGCCAGCCAGGAGCTG
AAAGAAGCAGTTAGGTCATCTGTAGAGGAAGAGCAGTGTTAGGAGTTAAGCGGGTTTGGGGA
GTAGGCTTGAGCCCTACCTTACACGCTGCTGATTATCAACATGTGCTTAAGCCAACATCCG
TCTCTTGAGCATGGTTTTTAGAGGCTACGAATAAGGCTATGAATAAGGGTTATCTTTAAGTC
TAAGGGATTCTGGGTGCCAGTCTCTCTTTCTCTACAGTCCATCTTCTGTTTCAACCAC
CCCACGTTACACATCCAGAATTCCTCTTTTACTGATAGTTTCTGTGCCAGGTTCTGGGC
TAAACCATGGAGATAAAAAGAGAGTAAAATACACTTCCCGACCTTAAGGATCTGAAA

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FIGURE 190

MAKMELSKAFSGQRTLLSAILSMLSLSFSTTSLLSNYWFVGTQKVPKPLCEKGLAAKCFDMP
VSLDGDNTSTQEVVQYNWETGDDRFSSFRSGMWLSCEETVEEPGERCRSFIELTPPAKR
GEKGLLEFATLQGPCHPTLRFGGKRLMEKASLPSPPLGLCGKNPMVIPGNADHLHRTS IHQL
PFATNRLATHWEPCLWAQTERLCCCFLCPVRSPGDGGPHDVFTSLPSCQLGSRRLTTTCLE
LWLGLLHGLALLHLLHGVGCHHLQHVVHQDGAGVQVQA

TOHETT-0th06660

AAC TGAAGGAAAGAAAGAAAGGTCAGCTTTGGCCCA**CATG**TGGTTACCCCTTGGTCTCTCTG
TCTTTATGTCTTTCTCCTCTTCTATTCTGTCACTCTCCCTCACTTAAGTCTCAGGCCGTGCA
GCAGCTCCTGTGGACATTGCCATCCCCTCTGGTAGCCTTCAGAGCAAAACAGGACAACCTATG
TTATGGATGTTTCCACCAACCAGGGTAGTGGCATGGAGACCCGTAACCATCTGTGCTTCTG
GATCTCTATGACAGAGCCACTTCTCCACCTCTGAAATGTTCCCTGCTCTGAAATCTGGCATG
AGATGGCACAGGTGACCACGCAGAAGCCACCAGAATCTTGCCTGCCCTATTCTCTCTCCAA
GTCTGTTCTCTTATTGTCAACCTCAGCACAAACAGGCTGGCGCCAATGGCATTACAGAGAAAG
CAATCTGTGTGGCTAGTGGGCAGATTACCATGCAAGCCCCAGGAGAAATGGAGGAGCTTTGT
AGCCACCTCCCTGTGACGCCAGTATTAACATGTCCCTTCCCCTGCCCGCCGCTAGATTGAG
GACATTGCGCCCTGTGTGCCACCAAAACCAGGACTTTCCCTTGGCTTGGCATCCCTGGCTCT
CTCCTGGTACCCAGCAAGACGCTGTGTTCCAGGGCAGTGTAGCATCTTTCAAGCTCCGTACT
ATGGCGATGGCCATGATGTTACAATCCCCTTGCTGAATAATCAAGTGGGAAGGGGAAGCA
GAGGGAAATGGGGCCATGTGAATGCAGCTGCTCTGTTCTCCCTACCTTGAGGAAAAACCAA
GGGAAGCAACAGGAACCTCTGCAACTGGTTTTTATCGGAAAGATCATCTTGCCTGCAGATGC
TGTTGAAGGGGCAACAAGAAATGTAGCTGGAGAAGATTGATGAAAGTCAGGTTGTAAGGAA
ATAGAACAGTCTGCTGGGAGTCAGACCTGGAATTCTGATCCAACTCTTTATTACTTTGGG
AAGTCACTCAGCCTCCCCGTAGCCATCTCAGGTTGACGGAACCCAGTGTATTACCTGCTGG
AACCAAGGAAACTAACATGTAGGTTACTAGTGAATACCCCAATGGTTTCTCCAATTATGCC
CAGTCCACCAAAAACAAATAAAACAAAATTCTCTAACACTGAAA

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FIGURE 192

MWLPLGLLSLCLSPILSSPSLKSQACQQLLWTLPSPLVAFRANRTTYVMDVSTNQSGME
HRNHLCFCDLYDRATSPPLKCSLL

00000000.11111111

FIGURE 193

GTAGCGCGTCTTGGGTCTCCGGCTGCGCGTGTGCGCGCGCGCGCTCGGGTCTGGAGCCAGGAGCGACGTCA
CGCGC**ATGG**CAGGAGCATAAAGCTTTGATTAGTTTGTCCCTTTGGAGGAGCAATCGGACTGATGTTTTGATGCTT
GGATGTGCCCTTCCAAATATACAACAATACTGCCCGCTTTGTTCTATTTTTTACATCTCTTCACTATTCC
ATACTGCATAGCAAGAGATTAGTGGATGATACAGATGCTATGAGTAACCTTTGTAAGGAACCTTGGCATCTTTTC
TTACACGGCGGATTTGCTGTGTGAGCTTTTGACTCCCTATTGATTGGCAGAGCACATCTGATTGAGTGGGGA
GCTTGTGCACTTGTCTCACAGGAACACAGTCATCTTTGCAACTATACTAGGCTTTTTCTTGGTCTTTGGAAG
CAATGACGAGCTTCAGCTGGCAGCAGTGG**TGA**AAAGAAATTAAGTGAATATGTCAAATGGACTTCCTGTCATT
GTGGCCATTACGACACACAGGAGATGGGGCAGTTAATGCTGAATGGTATAGCAAGCGCTTTGGGGGTAITTTA
GGTGCTCCCTTCTCACTTTTATTGTAAGCATACTATTTTCACAGAGACTTGCTGAAGGATTAAGGATTTTTCT
CTTTTGAAAAGCTTGACTGATTTACACTTATCTATAGTATGCTTTTTGTGGTGTCTGCTGAATTTAAATAT
TTATGTGTTTTCTGTAGGTTGATTTTTTTGGAAATCAATATGCAATGTTAAACACTTTTTTAATGTAATCA
TTTGCAATTGGTTAGGAATTAGAAATTCGCGCGGCTCTATTACTGGTCAAGTACATCTTTCTCTTAAATTAAT
TAGCTCCATTATACAAAAAATATAAAAATAAGTTTTCACTGAGTCAGGATGACATCACTCCCAATGTTATG
CAGACATACAGACGGTTGGCATACTGTTATAGACTGTATACTCAGTGCAAAATATAGCTGCATTTATACCTCAGAG
GGGCCAAGTGTAATGCCCATGCCCTCCGTTAAGGGTTGTTGGTTTTACTGGTAGACAGATGTTTTGTGGATTG
AAAAATTTTATGGAATTGCTACAGAGGAGTGCTTTCTCTCAATTGTTAGAAGAATTTATGTTAAACCTTA
AGGTAAGGGTGTAAAAACATTTTGAGATAAGGTTTTATTTATGTTTATTTATGTTAGAGTGAGTGCAATGT
GGGAGAAATGACATTGAATTCAGTTTTTGAATCCTGTTTCTATTTATAAGTGAATTTGTGATCTCCTATC
AACCTTTCATGTTTTACCTGTTTAAATGGACATACATGGAACCACTACTGATGAGGGACAGTTGATGTTTGC
ATCATATATGCCAGAAAACCTTCTCTGCTTCTCCTTTTGACTATTTGGTATGTTGTATATATTACATAAAAA
TAACTTTTCAATATAGTTTAATAACACTTAGAAGTGTTTACTTACCTGGAATAATGCTATGCCGTACATT
CAGAGTGCCCGCTCCCGCTGCAAGGCTTGCCATGATTAAACAGTAAGTTGTTAGTCTTACAGATAATTCATGCA
TTAACAGTTTAAGATTAGACCATGTAATAGTAGTCTTATTCTCTAAGGTTATATCATATGTAATTTAAAG
TATTTTTAAGACAAGTTTCTGTATACCTCTGAACCTGTTTGATTTTGAGTTTCATCATGATAGATCTGCTGTTT
CCTTATAAAAGGCATTTCTGTGTGAGTTAATGCAAGTAGCCAAAGTCCAGCTATATAGCAGCTTCAGAAACAT
ACCTGCACAAAATTCAGTAAACAGGCGATGATCAATTTATAGTGTGCTTTTACATCTAATAAATATCAGGA
CTTTTTTCAGGAGTGGGTATAAAAACATTCAGTTTGGTCTGACAGTATTTGTTAAGGATATTTGTTTGTATG
TTTTATCAGTATACCTTACATAAAAAATTTTCGCCATCAGCCAAAACCTCAGTAATCATGACAGCTCTGCTGTTG
TTTTATGAAGTTTATTTCTCAGAAAATGGGAATAAATTTGGGATTGTTGAGCTTTTTTACTAAAGATGCCATAA
AGCCACAGGTTTTATGCTTAACCTTAAGCCATGACTTTAGATATGAGATGACGGGAAGCAGACGAAATATCG
GCGTGTGCGCTGGAGCCTTCCATCGGAGGCTGAAAGTGGCTTTGTTGATTTAATGTTCAAGTTTCAAGAGAA
GGTGCAAGTACAGTATGAGTATCAGAGCTGGTGAGACAGTTGGGAACCTTTTGTGCTGTGATCTACTGGACTTT
TTTTTTCAGACAAGTGCAATTCAGTCTGGTCTTCCCTATTTTCTGTTCTGGATGTGCTGAGTGCAGTGCCTACTG
TTTTATCCACTTGGCCACAGACTTTTCTAACAGCTGCTATATTTCTATATACATAATGCAATGGCAGCAATT
GGTCTTTGACCTGTATACTAGCTTGACATAGTGTCTGTCTGATTCTAGGCTAGTTACTTGAGATATGAAT
TTTCCATAGAAATGCACTGATACACATTACCATCTCTCTATGAAAGAAAACTTTGATGATGAAACATAA
AGATTTTAAATATCTATTTTAAAAA

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FIGURE 194

MAGIKALISLSFGGAIGLMFLMLGICALPIYNKYWPLFVLFFYILSPIPYCIARRLVDDTDAM
SNACKELAIFLTGTGIVVSAFGLPIVFARAHLEWGACALVLTGNTVIFATILGFFLVFGSND
DFSWQQW

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[illegible]

FIGURE 196

MDFLLGLCLYWLLRRPSGVVLCLLGACFQMLPAAPSGCPQLCRCEGRLLYCEALNLTEAPH
NLSGLLGLSLRYNSLSELRAQQFTGLMQLTWLYLDHNHICSVQGDAFQKLRRVKELTLSSNQ
ITQLPNTTFRMPNLRSDLSYNKLQALAPDLFHGLRKLTTLHMRANAIQFVPVRIFQDCRS
LKFLDIGYNQLKSLARNSFAGLFKLTLEHNDLVKVNFAHFPRLLISLHSLCLRRNKVAIV
VSSLDWVWNLEKMDLSGNEIYMEPHVFETVPHLQSLQLDSNRITYIEPRILNSWKSITSIT
LAGNLWDCGRNVCALASWLSNFQGRYDGNLQCASPEYAQGEDVLDAVYAFHLCEDGAFTSG
HLLSAVTNRSDLGPPASSATTLADGGEGQHDGTFEPATVALPGGEHAENAVQIHKVVTGTMA
LIFSFLIVVLVLYVSWKCFPASLRQLRQCFVTQRRKQKQKQTMHQAAMSAQEYYVDYKPNH
IEGALVIINEYGSCTCHQQPARECEV

FIGURE 197

GTGCAAGGAGCCGAGGCGAG**ATG**GGCGTCCTGGGCGGGTCCTGCTGTGGCTGCAGCTCTGC
GCACTGACCCAGGCGGTCTCCAAACTCTGGGTCCCCAACACGGACTTCGACGTCGCAGCCAA
CTGGAGCCAGAACCAGACCCCGTGCGCCGGCGGCCTTGAGTTCCCGCGGACAAGATGG
TGTCAGTCCTGGTGCAAGAAGGTCACGCCGTCTCAGACATGCTCCTGCCGCTGGATGGGGAA
CTCGTCCTGGCTTCAGGAGCCGGATTGCGCGTCTCAGACGTGGGCTCGCACCTGGACTGTGG
CGCGGGCGAACCTGCCGTCTCCGCGACTCTGACCGCTTCTCCTGGCATGACCCGCACCTGT
GGCGCTCTGGGGACGAGGCACCTGGCCTCTTCTCGTGGACGCCGAGCGCGTGCCCTGCCGC
CACGACGACGTCTTCTTTCCGCCTAGTGCCTCCTTCCGCGTGGGGCTCGGCCCTGGCGCTAG
CCCCGTGCGTGTCGCGAGCATCTCGGCTCTGGGCCGACGTTACGCGCGACGAGGACCTGG
CTGTTTTCTTGGCGTCCCGCGCGGGCCGCCTACGCTTCCACGGGCCGGCGCGCT**TGA**GCGTG
GGCCCCGAGGACTGCGCGGACCCGTGGGCTGCGCTCTGCGGCAACGCGGAGGCGCAGCCGTG
GATCTGCGCGGCCCTGCTCCAGCCCCCT

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FIGURE 198

MGVLGRVLLWLQLCALTQAVSKLWVPNTDFDVAANWSQNRTPCAGGAVEFPADKMVSVLVQE
GHAVSDMLLPLDGELVLASGAGFGVSDVGSHLDCGAGEPAVFRDSDRFSWHDPHLWRS GDEA
PGLFFVDAERVPCRHDDVFFPPSASFRVGLGPGASPVVRVRSISALGRTFTRDEDLAVFLASR
AGRLRFHGP GALSVGPEDCADPSGCVCGNAEAQPWICAALLQP

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FIGURE 199

ATCGCATCAATTGGGAGTACCATCTTCCTCATGGGACCAGTGAAACAGCTGAAGCGAATGTT
TGAGCCTACTCGTTTGATTGCAACTATCATGGTGCTGTTGTGTTTTGCACTTACCCGTGTGTT
CTGCCTTTTGGTGGCATAACAAGGGACTTGCACTTATCTTCTGCATTTTGCAGTCTTTGGCA
TTGACGTGGTACAGCCTTTCCTTCATACCATTGCAAGGGATGCTGTGAAGAAGTGTTTTGC
CGTGTGCTTGCATTAATTTCATGGCCAGTTTTATGAAGCTTTGGAAGGCACATGGACAGAAG
CTGGTGGACAGTTTTGTAACTATCTTCGAAACCTCTGTCTTACAGACATGTGCCTTTTATCT
TGCAGCAATGTGTTGCTTGTGATTCTGAACATTTGAGGGTTACTTTTGAAGCAACAATACAT
TCTCGAACCTGAATGTGCTAGTACAGGATGAGAAGTGGGTTCTGTATCTTGTGGAGTGGAA
TCTTCCTCATGTACCTGTTTCCTCTCTGGATGTTGTCCCACTGAATCCCATGAATACAAAC
CTATTCAGCAACAGCAA
AAAAAAAAAAAAAAAAAAAAA

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FIGURE 200

MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGLALIFCILQSLALTWYSLSFIP
FARDAVKKCFVCLA

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FIGURE 201

TTGAGCGCAGGTGAGCTCTCGCGGTTCCGGGGCGTTCTCCAGTCAACCTCCCGCGGTACCGCGGCGCGCG
 CCAGAGGAGTCTCCTCCAGACCCCTCCCTCCGTTGCTCCAACTAATACGGACTGAACGGATCGCTCGAGGGT
 GGGAGAGAAAATTAGGGGAGAAAAGGACAGAGAGAGCACTACCATCCATAGCCAGATGATTATCTTACACTG
 AACTGATCAAGTACTTTGAAAATGACTTCGAAATTTATCTTGGTGCTTTCACTCTGCTGCACTGAGTCTTCT
 AACCACTTTTCTCTCCAATAGACCAGCAAAAGGTTCTACTAGTTTCTTTTGTGGATTTCGGTGGGATTACT
 TATATAAAGTTCCAAGCGCCCATTTTCACTATATATGAAATATGGTGTTCACTGAAGCAAGTTACTAATGTT
 TTTATTACAAAACCTACCTTAACCATTTACTTTGGTAACCTGGCCTCTTTGACAGAGAATCATGGGATTGTTGC
 AATGATATGTTTGTCTCTATTGGAACAAATCTTCTCCTTGGATCACATGAATATTTATGATTCGAAGTTT
 GGAAGAAGCGACACCAATATGGATCACAAACAGAGGGCAGGACATACATAGTGGTGCAGCCATGTGGCCCGGA
 ACAGATGTAAAAATACATAAGCGCTTCTCTACTCATACATGCCTTACAATGAGTCACTTTCAATTTGAAGATAG
 AGTTGCCAAATTTGTTGAATGTTTACGTCAAAAGAGCCCATAAATCTTGGTCTTCTCTATTGGGAAGACCTCG
 ATGACATGGGCCACCATTTGGGACCTGACAGTCCGCTCATGGGCGCTGTCAATTTGAGATATTGACAAGAAGTTA
 GGATATCTCATACAAATGCTGAAAAGGCAAGTTGTGGAACACTCTGAACCTAATCATCAAGTGATCATGG
 AATGACGCGAGTCTCTGAGGAAAGGTTAATAGAACTTGACAGTACCTGGATAAAGACCACTATAACCTGATTG
 ATCAATCTCCAGTAGCAGCCATCTTGCCAAAAGAGGTAATTTGATGAAGTCTATGAAGCACTAATCAAGCT
 CATCCTAATCTTACTGTTTACAAAAAGAGACGTTCCAGAAAGGTTGGCATTACAATACACAGTCGAATTC
 ACCAATCATAGCAGTGGCTGATGAAGGTTGGCACATTTTACAGATAAGTCAGATGACTTCTGTTAGGCAACC
 ACGGTTACGATAATGCGTTAGCAGATATGCATCCAATATTTTAGCCCATGGTCTGCTTCAGAAAGAATTTCT
 TCAAAAGAGCCATGAATCCACAGATTTGTACCCACTACTATGCCACCTCCTCAATATCACTGCCATGCCACA
 CAATGGATCATTTCTGGAATGTCCAGGATCTGCTCAATTCAGCAATGCCAAGGTTGGTCCCTTATACACAGAT
 CTATACTCCTCCTGGTAGTTAAACCCAGCAGAAATGACCAAGAGGGGTCATACCCCTTATTTATAGGGGTC
 TCTCTTGGCAGCATTTATAGTGATTGATTTTTTGTAAATTTTCAATAGCATTAAATTCACAGTCAAAATACCTGC
 CTTACAGATATGCATGCTGAAATAGCTCAACCATTTATACAAGCCTAATGTTACTTTGAAGTGGATTGTCATA
 TTGAAGTGGAGATTCATAAATATGTGCTAGTGTTTAAAGGTTTCAAATTTGGGAAACCGTTCCAACATCTGC
 AGAAACCATTAAGCAGTTACATATTTAGGTATACACACACACACACACACATACACACACACGACCAAA
 ATACTTACACTGCAAGGAATAAAGATGTGAGAGTATGCTCCATTGTTCACTGTAGCATAGGGATAGATAAG
 ATCCTGCTTATTTGGACTTGGCGCAGATAATGTATATATTTAGCACTTTGCACTATGATAAGTACCTTATAT
 ATTGCACTTTAAATTTCTCTCTGATGGGTACTTAAATTTGAAATGCACTTTATGGCAGTTATGCTTTATAAC
 TTGATTGAAATGACACACTTTTTCACCCATGTACAGAAATACITGTTACGCATTGTTCAAACCTGAAGGAAAT
 TCTAATAATCCCGAATAATGAACATAGAAATCTATCTCCATAAATTGAGAGAAGAAGAAGGTGATAAGTGTGA
 AAATTAATGTGATAACCTTTGAACCTTGAATTTGGAGATGTATTCCCAACAGCAGAAATGCAACTGTGGGCAT
 TTCTGTGCTTATTTCTTCCAGAGAAGCTGGTTTTCAATTTTTTCCCTCAAAGAGAGTCAAATACTGACAG
 ATTCGTTCTAAATATATGTTCTGTCAATAAAATATTGTGATTTCCCTGATGAGTCATATTACTGTGATTTC
 TAATAATGAAGACACCCATGAATACTTTTCTCTATATAGTCAGCAATGGCCTGAATAGAGCAACACGCA
 CCATCTCAGCATGTCTTCTCTGTGTTGTAATATTGCTCCTTTGAAAATTAATCACTATTAAATACATTAA
 AATCAATTTGGATAAAAAAAAAAAAAAAAAA

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FIGURE 202

MTSKFILVSFILAALSLSTTFSLQLDQQKVLVVSFDGFRWDYLYKVPTPHFHYIMKYGVHVK
QVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRKNKSFSLDHMNIYDSKFWEEATPIW
ITNQRAHGTSGAAMWPGTDVKIHKRFPTHYMPYNESVSFEDRVAKIVWFTSKEPINLGLLY
WEDPDDMGHHLGPDSPLMGPVISDIDKKLGYLIQMLKKAKLWNTLNLIITSDHGMTQCSEER
LIELDQYLDKDKHYTLIDQSPVAAILPKEGKFDEVYEALTHAHPNLTVYKKEDVPERWHYKYN
SRIQPIIAVADEGWHILQNKSDDFLLGNHGYDNALADMHPIFLAHGPAFRKNFSKEAMNSTD
LYPLLCHLLNITAMPHNGSFWNVQDLLNSAMP RVVPYTQSTILLPGSVKPAEYDQEGSYPYF
IGVSLGSIIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA

Signal Peptide:

amino acids 1-22

Transmembrane Domain:

amino acids 429-452

N-glycosylation sites:

amino acids 101-104, 158-161, 292-295, 329-332, 362-365, 369-372, 382-385, 389-392

Somatomedin B Domain:

amino acids 69-85

Sulfatase protein Region:

amino acids 212-241

GGATTTTTGTGATCCGGATTTCGCTCCACAGGCGGGACCTTTGTAACTCGGGGAGGCCCA
GACAGGCCCAACCTGCGGGCGGGAGGCAGCCGGGTGAGGGAGGTGAAGAAACCAAGACGC
AGAGAGGCCAAGCCCCCTTGCCTTGGTTCACACAGCCAAAGGAGGCAGAGCCAGAACTCACAA
CCAGATCCAGAGGCAACAGGGACATGGCCACCTGGGACGAAAGGCAGTCACCCGAGGGCC
AAGGTGGCTCCCGCTGAGAGGATGAGCAAGTTCTTAAGGCACCTCACGGTCGTGGGAGACGA
CTACCATGCCTGGAACATCAACTACAAGAAATGGGAGAATGAAGAGGAGGAGGAGGAGG
AGCAGCCACCACCACACCACTGCTCAGGCAGGAAGGCAGAGCTGCAGCCCTGACGTTGCC
CCTGCCCCTGCCCCGCACCCAGGGCCCCCTTGACTTCAGGGGCATGTTGAGGAAACTGTT
CAGCTCCACAGGTTTCAGGTCATCATCATCTGCTTGGTGGTTCTGGATGCCCTCCTGGTGC
TTGCTGAGCTCATCTGGACCTGAAGATCATCCAGCCGACAAGAATAACTATGCTGCCATG
GTATTCCTACTACATGAGATCACCATCTTGGTCTTTTTTATGATGGAGATCATCTTTAAATT
ATTTGTCTTCCGCTGAGTTCCTTACCACAAGTTTGAGATCCTGGATGCCCGTCGTGGTG
TGGTCTCATCTCATCTGGACATTGTCTCCTGTTCCAGGAGCACCAAGTTTGAGGCTCTGGG
CTGCTGATTCTGCTCCGGCTGTGGCGGGTGGCCCGGATCATCAATGGGATTATCATCTCAGT
TAAGACACGTTCAGAACGGCAACTCTTAAGGTAAAACAGATGAATGTACAATTGGCCGCCA
AGATTCAACACCTTGAGTTCAGCTGCTCTGAGAAGCCCTGGACTGATGAGTTTGCTGTATC
AACCTGTAAGGAGAAGCTCTCTCCGGATGGCTATGGGAATGAAAGAACTCCGACTCTACTCT
CACACAGCCACCGTGAAAGTCTTGAGTAAAATGTGCTGTACAGAAGAGAGAGAAGGAAG
CAGGCTGGCATGTTCACTGGGCTGGTGTTACGACGAGGAACCTGACAGTCACTGCGCCAGTTA
TCACTTCAGATTACAAATCACACAGAGTCATCTGCCTGTTTTCAATCACAAGAGAACAAACC
AAATCTATAAAGATATTCTGAAAAATATGACAGAATTTGACAAATAAAGCATAAACGTGTA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 204

MATWDEKAVTRRAKVAPAERMSKFLRHFTVVGGDYHAWNINYYKKWENEEEEEEQPPPTFV
SGEEGRAAAPDVAPAPGPAPRAPLDFRGMLRKLFSHRFQVIIICLVVLDALIVLAEILIDL
KIIQPDKNYYAMVFHYMSITILVFFMMEIIFKLFVFRLLSSFTTSLRSWMPVVVVVSFILDI
VLLFQEHQFEALGLLILLRLWRVARIINGIIISVKTRSERQLRLKQMNVLAAKIQHLEFS
CSEKPLD

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FIGURE 205

CGGCTCGAGCTCGAGCCGAATCGGCTCGAGGGGCAGTGGAGCACCCAGCAGGCGGCCAACAT
 GCTCTGTCTGTGCTGTACGTGCCGCTCATCGGGGAAGCCAGACCGAGTTCAGTACTTTTG
 AGTCGAAGGGGGCTCCCTGCCGAGCTGAAGTCCATTTCAAGCTCAGTGTCTTCATCCCTCC
 CAGGAATTTCCACCTACCGGCAGTGAAGCAGAAAAATTGTACAAGCTGGAGATAAGGACCT
 TGATGGGCAGCTAGACTTTTGAAGAATTTGTCCATTATCTCCAAGATCATGAGAAGAAGCTGA
 GGCTGGTGTAAAGATTTTGGACAAAAAAGATGATGGACGCAATTGACGGCAGGAGATCATG
 CAGTCCCTCGGGGACTGGGACTCAAGATATCTGAACAGCAGGCAGAAAAAATTTCAAGAG
 CATGGATAAAAAAGGCACGATGACCATCGACTGGAACGAGTGGAGAGACTACCACTCTCC
 ACCCGGTGGAAAAACATCCCCGAGATCATCTCTACTGGAAGCATTCACGATCTTTGATGTG
 GGTGAGAATCTAACGGTCCCGGATGAGTTTACAGTGGAGGAGAGGCAGACGGGGATGTGGTG
 GAGACACCTGGTGGCAGGAGGTGGGGCAGGGGCCGATCAGAACCTGCACGGCCCGCTGG
 ACAGGCTCAAGGTCTCATGAGGAGGAGGGCCAGTCACTCTGGCGGGGCAATGGCATCAA
 GGCTTCTCAGTCAATGATTCGAGAAGGAGGGCCAGTCACTCTGGCGGGGCAATGGCATCAA
 CGTCTTCAAAATTTGCCCGGATCAGCCATCAATTCATGGCCTATGAGCAGATCAAGCGCC
 TTGTTGGTAGTGACGAGGAGCTCTGAGGATTCAGCAGAGGCTTGTGGCAGGGTCTTTGGCA
 TGGGCTCAGGCTCGCCAGAGCAGCATCTACCAATGGAGGCTCTGAAGACCCGGATGGCGCTGG
 GAAGCAGGCGCAGTACTCAGGAATGCTGGACTGCCCAGGAGGATCTTGGCCAGGAGGGGG
 TGAGCGGCTTCTACAAGGCTATGTCCTCCCAACATGCTGGGCATCATCCCTATGCCCGCATC
 GACCTTGGCAGTCTACGAGGCTCAAGAATGCGCTGGCTCAGGCATGATGAGTGAACAGCGC
 GGACCTCCGGCTGTGTTGGTCTCTGGCCTGTGGCACCATGTCCAGTACCTGTGGCCAGCTGG
 CCAGCTTACCCTTGCCCTAGTCAGGACGCTCTTCAACATATCTCTGGCAGCAGGAGGGGGCTTCGGGGT
 CTCGAGGTGACCATGAGCAGCCTCTTCAACATATCTCTGGCAGCAGGAGGGGGCTTCGGGGT
 GTACAGGGGGCTGGCCCTCAACTTTCATGAAGTTCATCCAGCTGTGAGCATGAGCATGCTGG
 TCTACGAGAACCTGAGATCACCTGGGCGTGCAGTCCGGTTCAGGGGGGAGGGGGCGCCCG
 GCAGTGGACTCGCTGATCTGGGCGCAGCTGGGGTGTGCAAGCATCTATTCTGTGAATG
 TGCCAACACTAAGCTGTCTGAGCCAACTGTGAAAAACCTTAGACGACACCCGAGGAGGGT
 GGGGAGAGCTGGCAGGCGCAGGCTTGTCTGCTGACCCCAAGCAGACCTCTCTGTGGTTCC
 AGCGAAGACCAAGGACTTCTTAGGCTCCAGGCTCAGCAGGCTCCGGGCTCAGATGTGTAA
 GGCAGGACATTTTCTGAGCTGCTGCCAATAGTGAGCTTGGAGCCTGGAGGCCGGTTAGT
 TCTTCCATTTACCTTGCAGCAGCTGTTGGCCACGGCCCTGCCTCTGGTCTGCCGTGTC
 ATCTCCCTGTGCCCTTGTGCTGCTGCTGTCTGCTGAGGTAAAGTGGGAGGAGGGGTACAG
 CCCACATCCACCCCTCTGCTCCAATCCCATATCCATGATGAAGGTGAGGTACGCTGGCCT
 CCCAGGCTGACTTCCCAACCTACAGCATTGACGCCAATTTGGCTGTGAAGGAAGAGGAAG
 GATCTGGCTTGTGGTCACTGGCATGTAGCCCTGCTGATGGCTGGGGCTCTCGGGCATGCT
 TGGGAGTGCAGGGGCTCGGCTGCTGGCTGGCTGCACAGAAGGCAGTGTCTGGGGCTCA
 TGGTGTCTGAGCTGGCTTGCAGCCTGTGAGGATGGGCCCCACCTCAGAACCAAACTCAGT
 TCCCCACTGTGCGCATGAGGCGAGTGGAGCACCATTTGAGGGCGAAGGCGCAGAGCGTTTGT
 GTGTTCTGGGAGGGAAGGAAGGTTGGAGGCTTAATATGGACTGTTGGGAAAAGGG
 TTTTGTCCAGAAGGACAGCCGACAAATGAGCGACTTCTGTGCTTCCAGAGGAAGCAGGAG
 GAGCAGAGCTTGGCTGACTGCTCAGAGTGTGTTCTGAGCGCTGGGGGTTCTGTCCAAC
 CCGCAGGGCGCAGCGGGACAGCCACATTCACATGTGTGCTGATGTTGATGTGACTTATTT
 ATTTGTATTTTATTTGAACAGAGTTATGTCTCACTATTTTATAGATTTGTTTAAATTAATA
 CGTTGTCACTTTCAAGTTCATTTTTATTATATTATGTTGATGTTGATGTGACTTCC
 AAGCCCGCCAGTGGATGGGAGGAGGAGGAGAAGGGGGGCTTGGGCGCTCGAGTCACAT
 CTGTCCAGAGAAATCTCTTTGGGACTGGAGGCAGAAAAGCGGCGCAGGAGCAGCAGCTTG
 GTCCTCTCTTTTGGCAGTTTGGGGAAGGGCTTGGCCCGAGCTTAGGATTTACAGGGTTTGA
 CTGGGGGCTGGAGAGCAGGGAGGAACCTCAATAACCTTGAGGTGGAATTCAGTTATTTCT
 CTGCGCTCGAGGGTTCTTTATTTTCACTCTTTTCTGAATGTCAAGGCAGTGGGTGGCTCT
 CACTGTGAATTTTGTGGGGGGGGGGTGGAGGAGAGGGTGGGGGGTGGCTCGCTCCCTCC
 CAGCTTCTGCTGCCCTTGCTTAACAAATGCCGGCCAACTGGGCACCTCAGGTTGCACTTCC
 ATTCACCAAGATCACTGATGAGGAATCTTCAATAGGATCAAAAGATCAATGCAAAATTT
 GTTATGATTAACATTAACCTGAGTGTGTCAAAAAGCAAAATTAAGAAAGAAATGGACGTAG
 AAGTTGTATTTAAAGCAGCTTCTAATAAAGTTGTTTCAAGCTGAAAAAAGAAAAA
 AA

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FIGURE 206

MLCLCLYVPVIGEAQTEFQYFESKGLPAELKSIFKLSVFIPSQEFSTYRQWKQKIVQAGDKD
 LDGQLDFEEFVHYLQDHEKKLRLVFKILDKKNDGRIDAQEIMQSLRDLGVKISEQQAEKILK
 SMDKNGTMTIDWNEWRDYHLLHPVENIPEIILYWKHSTIFDVGENLTPDEFTVEERQTGMW
 WRHLVAGGAGAVSRTCTAPLDRCLKVLMQVHASRSNNMGIVGGFTQMIREGGARSLWRGNGI
 NVLKIAPESAIFMAYEQIKRLVGSQETLRIHERLVAGSLAGATAQSSIYPMEVLKTRMAL
 RKTGOYSGMLDCARRILAREGVAAFYKGYVPNMLGIIPYAGIDLAVYETLKNAWLQHYAVNS
 ADPGVFVLLACGTMSSTCGQLASYPLALVRTRMQAQASIEGAPEVTMSSLFKHILRTEGAFG
 LYRGLAPNFMKVIPAVSISYVVYENLKITLGVQSR

Important features:**Signal peptide:**

amino acids 1-16

Transmembrane domain:

amino acids 284-304, 339-360, 376-394

Mitochondrial energy transfer proteins signature.

amino acids 206-215, 300-309

N-glycosylation site.

amino acids 129-133, 169-173

Elongation Factor-hand calcium-binding protein.

amino acids 54-73, 85-104, 121-140

FIGURE 207

GGAAGGCAGCGGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCCAGCC**AT**
GGCTTCCCTGGGGCAGATCCCTCTTCTGGAGCATAATTAGCATCATCATTATTCTGGCTGGAG
 CAATTGCACTCATCATTGGCTTTGGTATTTACGGGAGACACTCCATCACAGTCACTACTGTC
 GCCTCAGCTGGGAACATTGGGGAGGATGGAATCCTGAGCTGCACCTTTGAACCTGACATCAA
 ACTTTCGTGATATCGTGATACAATGGCTGAAGGAAGGTGTTTTAGGCTTGGTCCATGAGTTCA
 AAGAAGGC AAAAGATGAGCTGTCGGAGCAGGATGAAATGTTT CAGAGGCCGGACAGCAGTGTTT
 GCTGATCAAGTGATAGTTGGCAATGCCTCTTTGCGGCTGAAAAACGTGCAACTCACAGATGC
 TGGCACCTACAAATGTTATATCATCACTTCTAAAGGCAAGGGGAATGCTAACCTTGAGTATA
 AAATGGAGCCTTCAGCATGCCGGAAGTGAATGTGGACTATAATGCCAGCTCAGAGACCTTG
 CGGTGTGAGGCTCCCCGATGGTTCCCCAGCCACAGTGGTCTGGGCATCCAAGTTGACCA
 GGGAGCCAACCTCTCGGAAGTCTCCAATACCAGCTTTGAGCTGAACTCTGAGAATGTGACCA
 TGAAGGTTGTGCTGTGCTCTACAATGTTACGATCAACAACACATACTCCTGTATGATTGAA
 AATGACATTGCCAAAGCAACAGGGGATATCAAAGTGACAGAATCGGAGATCAAAAGGCGGAG
 TCACCTACAGCTGCTAAACTCAAAGGCTTCTCTGTGTGCTCTCTCTTTCTTTTGCCATCAGCT
 GGGCACTTCTGCCTCTCAGCCCTTACCTGATGCTAAAA**TAA**TGTGCCTTGGCCACAAAAAG
 CATGCAAAGTCATTGTTACAACAGGATCTACAGAACTATTTCAACCACAGATATGACCTAG
 TTTTATATTTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTGAGCAACAAGAGCA
 AGAAACAAAAAGAAGCCAAAAGCAGAAGGCTCCAATATGAACAAGATAAATCTATCTTCAAA
 GACATATTAGAAGTTGGGAAAAATAATTCATGTGAAC TAGACAAGTGTGTTAAGAGTGATAAG
 TAAATGCACGTGGAGACAAGTGCATCCCCAGATCTCAGGGACCTCCCCCTGCCTGTACCT
 GGGGAGTGAGAGGACAGGATAGTGCATGTTCTTTGTCTCTGAATTTTTAGTTATATGTGCTG
 TAATGTTGCTCTGAGGAAGCCCTTGAAAGTCTATCCCAACATATCCACATCTTATATTTCCA
 CAAATTAAGCTGTAGTATGTACCCTAAGACGCTGCTAATTGACTGCCACTTCGCAACTCAGG
 GCGGCTGCATTTTAGTAATGGGTCAAATGATTCACCTTTTATGATGCTTCCAAGGTGCCT
 TGGCTTCTCTTCCCAACTGACAAATGCCAAAGTTGAGAAAAATGATCATAATTTTAGCATAA
 ACAGAGCAGTCGGGGACACCGATTTTATAAATAAACTGAGCACCTTCTTTTAAACAAAAAA
 AA

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FIGURE 208

MASLGQILFWSIISIIIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDI
KLSDIVIQWLKEGVLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASRLRLKNVQLTD
AGTYKCYIITSKGGKGNANLEYKTGAFSMPEVNVVDYNASSETLRCEAPRWFPQPTVVWASQVD
QGANFSEVSNTSFELNSENVMTKVVSVLNVNTINNTYSCMIENDIAKATGDIKVTSESEIKRR
SHLQLLSKASLCVSSFFAISWALLPLSPYMLK

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[illegible]

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FIGURE 210

MAASLGQVLALVLVAALWGGTQPLLKRASAGLQRVHEPTWAQQLQEMKTLFLNTEYLMPFLL
LNQCGSLLYLTLASTDLTLAVPICNSLAIIFTLIVGKALGEDIGGKRKLDYCECGTQLCGS
RHTCVSSFPEPISPEWVRTRPFPILPFPLQLFCFLVAIRVPFPWTVWRKTEAGVWD

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FIGURE 211

CTTCTGTAGGACAGTCACCAGGCCAGATCCAGAAGCCTCTCTAGGCTCCAGCTTTCTCTGTG
GAAGATGACAGCAATTATAGCAGGACCCCTGCCAGGCTGTCGAAAAGATTCCGCAATAAACT
TTGCCAGTGGGAAGTACCTAGTGAAACGGCCTAAGATGCCACTTCTTCTCATGTCCCAGGCT
TGAGGCCCTGTGGTCCCCATCCTTGGGAGAAGTCAGCTCCAGCACCATGAAGGGCATCCTCG
TTGCTGGTATCACTGCAGTGCTTGTGTCAGCTGTAGAATCTCTGAGCTGCGTGCAGTGTAAT
TCATGGGAAAAATCCTGTGTCAACAGCATTGCCTCTGAATGTCCCTCACATGCCAACACCAG
CTGTATCAGCTCCTCAGCCAGCTCCTCTCTAGAGACACCAGTCAGATTATACCAGAATATGT
TCTGCTCAGCGGAGAACTGCAGTGAGGAGACACATTACAGCCTTCACTGTCCACGTGTCT
GCTGAAGAACACTTTCATTTTGTAAAGCCAGTGCTGCCAAGGAAAGGAATGCAGCAACACCAG
CGATGCCCTGGACCCCTCCCCTGAAGAACGTGTCCAGCAACGCAGAGTGCCCTGCTTGTATG
AATCTAATGGAACCTCCTGTCGTGGGAAGCCCTGAAATGCTATGAAGAAGACAGTGTGTC
TTTCTAGTTGCAGAACTTAAGAATGACATTGAGTCTAAGAGTCTCGTGCTGAAAGGCTGTTT
CAACGTCACTAACGCCACCTGTCAGTTCCTGTCTGGTGAAAAACAAGACTCTTGGAGGAGTCA
TCTTTCGAAAGTTTGTAGTGTGCAAAATGTAAACAGCTTAACCCCCACGCTGCACCAACCACT
TCCCACAACGTGGGCTCCAAAGCTTCCCTCTACCTCTTGGCCCTTGCCAGCCTCCTTCTTCG
GGGACTGCTGCCCCTGAGGTCTTGGGGCTGCACCTTGCCAGCAGCCCCATTTCTGCTTCTCTG
AGGTCCAGAGCAGCCCTGCGGTGCTGACACCTCTTTCCTGCTCTGCCCGGTTTAAGTGC
CCAGTAAGTGGGAGTCACAGGTCTCCAGGCAATGCCGACAGCTGCCTTGTCTTTCATTATTA
AAGCACTGGTTCATTCACTGCCAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 213

GGCCTCGGTTCAAACGACCCGGTGGGTCTACAGCGGAAGGGAGGAGCGAAGGTAGGAGGCA
 GGGCTTGCCCTCACTGGCCACCCTCCCAACCCCAAGAGCCCAGCCCC**ATG**GTTCCCGCCGCCG
 GCGCGCTGCTGTGGGTCTCTGCTGAATCTGGGTCCCCGGGCGGGGGGCCAAGGCCTG
 ACCCAGACTCCGACCGAAATGCAGCGGGTCAGTTTACGCTTTGGGGGCCCCATGACCCGCAG
 CTACCGGAGCACCGCCGGACTGGTCTTCCCCGGAAGACAAGGATAATCCTAGAGGACGAGA
 ATGATGCCATGGCCGACGCCGACCGCTGGCTGGACCAGCGGCTGCCGAGCTCTTGGCCGCC
 ACGGTGTCCACCGGCTTTAGCCGGTCTGTCGCCATTAAACGAGGAGGATGGGTCTTCAGAAGA
 GGGGGTTGTGATTAATGCCGGAAGGATAGCACCAGCAGAGAGCTTCCAGTGCGACTCCCA
 ATACAGCGGGGAGTTCCAGCACGAGGTTTATAGCCAATAGTCAGGAGCCTGAAATCAGGCTG
 ACTTCAAGCCTGCCGCGCTCCCCGGGAGGTCTACTGAGGACCTGCCAGGCTCGCAGGCCAC
 CCTGAGCCAGTGGTCCACACCTGGGTCTACCCGAGCCGGTGGCCGTACCCTCACCCACAG
 CCATGCCATCTCCTGAGGATCTGCGGTGGTGTGATGCCCTGGGGCCCGTGGCACTGCCAC
 TGCAGTTCGGGCACCATGAGCCGGAGCCGGTCTGGGAAGCTGCACGGCCCTTCCGGGCGCCT
 TCGAGTTGGGGCGCTGAGCCAGCTCCGCACGGAGCACAAAGCCTTGACCTATCAACAATGTC
 CCTGCAACCGACTTCGGGAAGAGTGCCCCCTGGACACAAGTCTCTGTACTGACACCACTGT
 GCCTCTCAGAGCACCAACAGTACCAGGACCACCACTACCCCTTCCCCACCATCCACCTCAG
 AAGCAGTCCCAGCCTGCCACCCGCCAGCCCTGCCAGCCCTGGCTTTTGGAAACGGGTCA
 GGATTGGCCTGGAGGATATTTGGAATAGCCTCTCTTCAGTGTTCACAGAGATGCAACCAATA
 GACAGAAACAGAGG**TAA**TGGCCACTTCATCCACATGAGGAGATGTAGTATCTCAACCTCT
 CTGCCCCTTTCAATCCTAGCACCCACTAGATATTTTGTAGTACAGAAAAACAAACTGGAAAA
 CACAA

FIGURE 214

MVPAAGALLWVLLNLGPRAAGAQGLTQTPTEMQRVSLRFGGPMTRSYRSTARTGLPRKTRI
ILEDENDAMADADRLAGPAAAEELLAATVSTGFSSSAINEDGSSEEGVVINAGKDSTSREL
PSATPNTAGSSSTRFIANSQEPEIRLTSSLPSPRSTEDLPGSQATLSQWSTPGSTPSRWP
SPSPTAMPSPEDLRLVLMFWGFWHCHCKSGTMSRSRSGKLHGLSGRLRVGALSQLRTEHKPC
TYQQCPCNRLREECPLDTSLCDTNCASQSTTSTRTTTTTFPTIHLRSSPSLPPASPCPALA
FWKRVRIGLEDIWNLSVVFTEMQPIDRNQR

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CCGGGTGCACCAACGGCTCGGGGAGAAAGGATGGCCGGCTGGCGGCGGGTGTGTCTCGGTACGTCGGGCA
CGGGCGCTGGCGAGCGCTCGACGGGCGACCGTAGCCCGTCCGTCAGCGCATCGCTACGTCGAGTCGGAAGASCA
GAACTGCTCTGGGGGCGCTCTGAATCACTTCGCTCGCTCGGCGACCAATCTACATGAGTCTGACAGSGTCAGCT
CTGCGGACGACTCTAAGTATGATGATGTGGGTCACTGTGGGCTACCTCTACGGAAGGTCAACAAGTGCCT
GAGTTCACTCGGAAGTGGCCCTTCGCGGTCTCTGTCTTTCAAGAGCGGCATCGGAGCGGCCCTGTTTCT
CAATGGCTCGGGACCGCTGGTATGCTCTGGCGTACCGACACTCTGTGTCAGGCCCTCTCCCCATGTACCA
CTGTGTGGCTTCGCTGGTGGTGTCCTCAATCATGATGTTCTGTGTCACAGTCTTCACACACAGGACCATG
CTCAGAGAAATATGGACTACTCTGTGGCTCCAGTCTCATCTACCATCACTCACTACTCTGCTGCTCAGGAC
CTGGGGCTGCAGCACCCAGCTGTGTGATGCTCTCGGGCTCTCTGCTGCTCATGTGACCGTGCAGCTCT
CTACTTGAGCTCTATCCGCTCTGACATCTGCTCAACCTGTGGCCACCTGGCATTTGGCTGGTCAACGCT
GTGTGGTGGCTGGCCCTGGTGTCTGTGAACACGCGGCCCTGCTCATGCTGCAGTGGCTGGTGTGTGTTCT
GCTGCTCAGAGGGCTGCATCTGCTGAGCTGCTTACTCTCCACCGTCTCTGGGTGTCTGGATGGCATGCCA
CTTGCACATCAGCATGCATCCCTGTCCAGCTCTCTTTTACTGTTTCTGGAAGTACAGCTCTGACTGTCT
AAGAACTCAGAGGACAAGTTCAAGTGTACGCTGAAGACTCTGGAGCGAGTCTGCCCGATGGGATCTGCCCC
CGCCTGTGGCCTCCCTCTCCCTCAACCTTGAGATGATTTTCTCTTTCAACTCTTGAATCTTGACATGA
AGGATGTGGGCGAGAATCATGTGGCCAGGCCACCCCTGTTGGCCTCAACGCTCTGGAGTGTGTTCTAGG
AAGGCTCCACAGATCTGGGACTCGAGTGGGACGGCTCTACTCTTGAGACTGAATGGGGTGAATCA
GTGTGTTCTTAGCTCTACCGGAGGACAGCTGGTGTCTTCTCCACACAGCTCTCCCTCCCATCTGCCCAGT
CTGGCTGGGTCTGAAGCCCTCTGTCTACTCGGAGACAGGAGACACAGCCCTTAGGATACAGGGGGTCTCC
TCTGTGTACACCCCCCACTCTCTCCAGGACACCATTAAGTGGTGTGTGATCTGTGTTTGGGCAACGAA
GGTTCAAGGCGATCTCCCATGGGATCTGAGGAGCAAGCTGTGGGATGGGAAGGATTTCACTACCGTCA
GTGTGCCCTACAGCAGGTTCCAGGAGGCTCTACCATCTCCCTTTACGGGCGAGGCTCAGAGCGCTCAGGCA
AGGATCTGTGTGCTGTGTGTGTGAGAGCTGCCACCTGTGTGCGGAGTGTGGGCGAGCTGAGTGCATAG
TCAGAGGGCGCTGAGCATGGGCTGGGTGTGTGTGATCTCAGGCGTAGTGCAGCATGTGGAGCGGGTGTGT
CGGGAGAGAGGTGTGGCTTCAAGTGTGTGTGTGTCAGGGGGTGGTGTGTAGCTGGGTTAGGGGAACTGTG
TGCGGCTGTGTGGCATGTGAGATGATGACTCGCGGTGAATGTGTCCACAGTGTAGAGAGTGTGGACAGGT
GGGGAATCTGTACCATTAATTAATCACTTGTGAGGCGCAGCTCTGCCAGAGACGGCACTGGGCGGACAG
CAGGAGCTCTTCATCAGCAGGCTGCTGTGTGATGTGTCCCTGTGTGGCCCTTTGGCCGCTCTCTGCAAA
CTCAGAGGTTCCCCACAGCAAGTGCCTTCAGAGACAGCCCTCGGAGCAGAGGAGGAATAATGGGATGCG
TGGGGCTCTTCATCTCTCTTTTCTTGCTGCTCTGCATGCTGGCTGGCCTCTCCCTCCAAACCTCTATCTCCCT
CTGCCAGCCGCTTTGCTACGCTGATTTTGGGAGAGGAGAGGGGCGATTTAGGAGGAGGGGGAGAAAGT
TATGGCTGGGTGTGTTTCTTCTCTCCAGAGGGTCTTACTGTCTCAGGTTGGCCCGAGGAGGAGCGGGGG
ACATATCTGCTGTGGCTGTAAGAAGTGCACCTGCAATTTACAGACAGCTGCGATGTCTGCTGCCACAGG
AATAGATGTAGGAGGGGCTCCAGAAATTTTCATCCCAAGGCACTCTCGGTGGTTGAGAGCAATGTGATTTTGT
CTCTGCCCTTGACCCCTGTGCTCTCTTTGAGGAGGGGAGCTATGCTACCATCCAACCTCAGGAGCTCGGTGT
GCTTCGCTGAGTCTTTTGTATCTGAAACCTTTAAGTGGGAGGTTGGCAAGGATGTGCTTTAATAATCAA
TTACAGGCTCAAAAAAATAAAAAA

FIGURE 216

MAGLAARLVLLAGAAALASGSQGDREPVYRDCVLQCEEQNCSSGGALNHFRSRQPIYMSLAGW
 TCRDDCKYECMWVTVGLYLQEGHKVPQFHGKWPFSRFLFFQEPASAVASFLNGLASLVMLCR
 YRTFVPASSPMYHTCVAFAWVSLNAFWSTVFHTRDTDLTEKMDYFCASTVILHSIYLCCVR
 TVGLQHPAVVSAFRALLLLMLTVHVSYSLSLIRFDYGYNLVANVAIGLVNVVWWLAWCLWNQR
 RLPHVVRKCVVVVLLQGLSLLELLDFPPLFWVLDAAHAIWHISTIPVHVLFSSFLEDDSLYLL
 KESDKFKLD

Important features:**Signal peptide:**

amino acids 1-20

Transmembrane domains:

amino acids 105-123, 138-156, 169-185, 193-209, 221-240, 256-272

N-glycosylation site.

amino acids 40-44

N-myristoylation site.

amino acids 43-49

CUB domain proteins profile.

amino acids 285-302

Amiloride-sensitive sodium channels proteins.

amino acids 162-186

FIGURE 217

GGCCGCCTGGAATTGTGGGAGTTGTGTCTGCCACTCGGCTGCCGGAGGCCGAAGGTCCGTGA
 CTATGCTCTCCCAGAGCCTGCCTTCATCTAGGATGGCTCCTCTGGGCATGCTGCTTGGGCTG
 CTGATGGCCGCTGCTTCACCTTCTGCCTCAGTCATCAGAACCTGAAGGAGTTTGCCCTGAC
 CAACCCAGAGAAGAGCAGCACCAAGAAACGGAGAGAAAAGAAACCAAGCCGAGGAGGAGC
 TGGATGCCGAAGTCTTGAGGTGTTCCACCCGACGCATGAGTGGCAGGCCCTTCAGCCAGGG
 CAGGCTGTCCCTGCAGGATFCCACGTACGGCTGAATCTTCAGACTGGGGAAGAGAGGCCAAA
 ACTCCAATATGAGGACAAGTTCGAAATAATTGAAAGGCAAAGGCTGGATATCAACACCA
 ACACCTACACATCTCAGGATCTCAAGAGTGCCTGGCAAATTCAGGAGGGGGCAGAGATG
 GAGAGTTCAAAGGAAGACAAGGCAAGGCAGGCTGAGGTAAAGCGGCTCTTCCGCCCCATTGA
 GGAAGTGAAGAAAGACTTTGATGAGCTGAATGTTGTGCTATTGAGACTGACATGCAGATCATGG
 TACGGCTGATCAACAAGTTCAATAGTTCACGCTCCAGTTTGAAGAGAAGATTGCTGCGCTC
 TTTGATCTTGAATATATGTCATCAGATGGACAATGCGCAGGACCTGCTTTCCCTTGGTGG
 TCTTCAAGTGGTGATCAATGGGCTGAACAGCACAGAGCCCTCGTGAAGGAGTATGCTGCGT
 TTGTGCTGGGCGCTGCCTTTTCCAGCAACCCCAAGGTCAGGTGGAGGCCATCGAAGGGGGA
 GCCTGCAGAAGCTGCTGGTCATCCTGGCCACGGAGCAGCCGCTCACTGCAAGAAAGAGGT
 CCTGTTGCACTGTGCTCCCTGCTGCGCCACTTCCCTATGCCCAGCGGCACTTCTGAAGC
 TCGGGGGGCTGCAGGTCTTGAGGACCTGGTGCAGGAGAAGGGCACGGAGGTGCTCGCCGTG
 CGCGTGGTCACACTGCTCTACGACCTGGTCACGGAGAAGATGTTGCCCAGGAGGAGGCTGA
 GCTGACCCAGGAGATGTCCCAGAGAAGCTGCAGCAGTATCGCCAGGTACACCTCCTGCCAG
 GCCTGTGGGAACAGGGCTGGTGCGAGATCACGGCCCCACCTCCTGGCGTGCCCGAGCATGAT
 GCCCGTGAGAAGGTGCTGCAGACACTGGGCGTCTCCTGACCACCTGCCGGGACCGCTACCG
 TCAGGACCCCCAGCTCGGCAGGACACTGGCCAGCCTGCAGGCTGAGTACCAGGTGCTGGCCA
 GCCTGGAGCTGCAGGATGGTGAGGACGAGGGCTACTTCAGGAGCTGCTGGGCTCTGTCAAC
 AGCTTGCTGAAGGAGCTGAGATGAGGCCCCACACCAGGACTGGACTGGGATGCCGCTAGTGA
 GGCTGAGGGGTGCCAGCTGGGTGGGCTTCTCAGGCAAGGAGACATCTTGGCAGTGCTGGCT
 TGCCCATTAATGGAACCTGAAGGCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
 AA

 0909040 11401
 104111 040660

FIGURE 218

MAPQSLPSSRMAPLGMLLGLMAACFTFCLSHQNLKEFALTNPEKSSSTKETERKETKAEHEEL
 DAEVLEVFPHTHEWQALQPGQAVPAGSHVRLNLQTGEREAKLQYEDKFRNNLKGKRLDINTN
 TYTSQDLKSALAKFKEGAEMESSKEDKARQAEVKRLFRPIEELKKDFDELNVVIETDMQIMV
 RLINKFNSSSSSLEEKIAALFDLEYVYVHQMDNAQDLLSFGGLQVVINGLNSTEPLVKEYAAF
 VLGAAFSSNPVKVQVEAIEGGALQKLLVILATEQPLTAKKKVLFALCSLLRHFPYAQRQFLKL
 GGLQVLRITLVQEKGEVLAVRVVTLTYDLVTEKMFEEEEAELTQEMSPEKLQQYRQVHLLPG
 LWEQGWCEITAHLALLPEHDAREKVLQTLGVLLTTCRDRYRQDPQLGRTLASLQAEYQVLAS
 LEIQDGEDEGYFQELLGSVNSLLKELR

Important features:**Signal peptide:**

amino acids 1-29

Hypothetical YJL126w/YLR351c/yhcX family protein.

amino acids 364-373

N-glycosylation site.

amino acids 193-197, 236-240

N-myristoylation site.

amino acids 15-21, 19-25, 234-240, 251-257, 402-408, 451-457

Homologous region SLS1 protein.

amino acids 68-340

TTCCGGCTTCCGTAGAGGAAGTGGCGCGGACCTTCATTTGGGGTTTCGGTTCCCCCCTTCCCTCCGCGGGGTTCGGGGTGACATTGCACCGCGCCCTCGTGGGGTCGCGTTGCCACCCCA
CGGGACATCCCCAGCTGGCGCGCCCTCCCATTTGCCTTGCTCTGGTCAGGCCCCACCCCC
TTCCACCTTGACACAGC**ATGGG**GGGCTGCGGTGTTTTTGGGCTGCACATTTCGTCTGGGTTCGGC
CCGGCCTTCGGCGCTTTTCTTGATCACTGTGGCTGGGAGCCCGCTTCGGTTATCATCTCTGGT
CGAGGGGACATTTTTCGGCTGGCTTCCCTGCTCTGGCCCTGTGGTCTGGTTCACTCTTG
TCCATTGACACCGACCGCTCAGATGCCCGGCTCAGATACGGCTCCTGATTTTGTGTGCTGT
GTCTGTCTCTTCTACAGGAGGTGTTTCGGTTTGCCTACTACAAGTGCCTTAAGAAGCGAG
TGAAGGGTTAGCATCGCTGAGTGAGGACGGAAGATCACCATCTCCATCCGCCAGATGGCCT
ATGTTTCTGGTCTCTCTTCGGTATCATAGTGGTGTCTCTCTGTTATCAATATTTTGGGT
GATGCACTTGGGCGAGGTGTGGTGGGATCATAGAGACTACCCATTACTTCTGACTTC
AGCCTTCTGACAGCAGCCATTATCTGCTCCATACCTTTTGGGAGTGTGTGTTTGTATG
CCTGTGAGAGGAGACGACTGGGCTTTGGGCTGTGGTGTGGGAGTCCACTACTGACATCG
GGACTGACATTTCTGAACCTCGGTATGAGGCGACCGTGTCTGCCCATTAATGACGTACTGT
TTCTATGGGGCTCTGGGCGCTTCATCACAGCTGAGGGGTCCCTCCGAAGTATTACGCGACGCC
TTCGTGTGAAGGACT**TGA**TCACTTGACTGATCGGCTGACAGATCCCACTGCTCTGCCATG
CCCATGACTGAGCCGACGCCAGCCCGGCTTCATTGCCACATTTCTGTCTCCTTCTCGT
GGTCTACCCCACTACCTCTCCAGGTTTGTGTTTGTCTCTGTTGACCGGTAGTCTCTAAGCTT
TACCAGGACGAGCTGGGTTGACCGAGTCACTGAGTGTGGGTTTGAATCTGCATTTATCC
CACCACCTGGGACCCCTTGTGTGTCCAGGACTCCCCCTGTGTGAGTGTCTGTCTCAC
CTCGCCCAAGACTACCTCCTTCCCCCTCTGACGGCCAGCGCAGGAGGACATCGGGGTGAT
GGTGATTCTGCCCTGCGCATCCCAACCGAGACTGAGGGAACCTAGGGGAGCCCTGGGC
CTGGGGTGCCCTCTGATGTCTCGCCCTGATTTCCTCATCTCCAGTCTCGGACATGCGAG
GTTGCCAAGAAAGGACCTAGTTTAGCCATTGCCCTGGAGATGAATTAATGAGGCTCA
GGATAGATTGAGCTCTGAGTTTCTCAGATCTCCCTCAAGACTGGACATCTTGGTCTTTTCTC
AGGCTCGAGGGGAGAACATTTTGTGTGTGATATAAATACCTAACTGCTTTTTCCTTTTTT
GAGGTGGGGGAGGAGGAGGATATATTGGAATCTTCTAACCTCTGCTGGGTATATTTTCTC
TCCTCGAGTTGCTCCTCATGGCTGGCTCATTTCGGTCCCTTTCTCTCTGGTCCCGACCTT
GGGGGAAAGGAAGGAAGTGATCTTTTGGGAACGTGCATCTGGAATCAATGTGTTTAACTC
CCTTAACCAACGAGCATCTCTCTCCCCAAGGTGAAGTGAGGGGTGCTGTGGTGAGCTGGC
CACTCCAGAGCTCGAGTGCCACTGGAGGATCAGACTACCATGACATCGTAGGAGGAGGG
GAGATTTTTTTGTAGTTTTTAATTGGGGTGTGGAGGGCGGGAGGTTTCTATAAATGT
ATCATTTTCTGCTGAGGGTGGAGTGTCCCATCTTTTAATCAAGGTGATTGTGATTTTGACT
ATAAAAAAAGAAATTTGTAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA
AAAAA

FIGURE 220

MGAAVFFGCTFVAFGPAFALFLITVAGDPLRVIIILVAGAFFWLVSLLLASVVWFILVHVTDR
SDARLQYGLLIFGAAVSVLLQEVRFRFAYYKLLKKADEGLASLSEGRSPISIRQMAYVSGLS
FGIISGVFSVINILADALGPGVVGIIHGDSPIYFLTSAFLTAAIILLHTFWGVVFFDACERRR
YWALGLVVGSHLLTSGLTFLNPWYEASLLPIYAVTVSMGLWAFITAGGSLRSIQRSLCKD

FOHETT" 04406660

FIGURE 221

AAGCTGGTTTAAGGAAGCAGAGGAGGGTTAGATTGAGTGAGGACGGAAGATCAACCCA
TTTCCATTCCGCCAGATGGCCTATGTTTCTGGTCTCTCCCTTCGGNATCATCAGTGGTGTNT
TNTCTGTTATCAATATTTTGGCTGATGCANTTGGGCCAGGTGTGGTTGGGATCCATGGAGAC
TCACCCCTATTANTTCCTGANTTCAGCCTTTNTGACAGCAGCCATTATCCTGCTC

0990442.111401

FIGURE 222

GACCGACCGTTCAGATGCCCGGTTCCAGTACGGCTTCCTGATTTTTGGTGCTGCTGNTCTG
TCCTTCTACAGGAGGTGTTCCGCTTTGCCTANTACAAGCTGCTTAAGAAGGCAGATGAGGGG
TTAGCATNGCTGAGTGAGGACGGAAGATCACCCATTTCCATCCGCCAGATGGCCTATGTTTN
TGGTNTTTCCTTCGGTATCATCAGTGGTGTTTTNTCTGTTATCAATATTTGNTGATGCAN
TTGGGCCAGGTGTGGTTGGGATCCATGGAGANTCACCTATTAATTCCTGAATTCAGCCTTT
NTGACAGCAGCCATTATCCTGNTCCATACCTTTTGGGGAGTTGTGTTTTTTGATGCCTGTGA
GAGGAG

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FIGURE 223

NGTTGGAGAAGTGGCGCGGACNTTCATTTGGGGTTTCGGTTTCCCCCTTTCCCTTTCCCCG
GGGTCTGGGGTGACATTGCACGGGCCCTCGTGGGGTCGCGTTGCCACCCACGCGGACTCC
CCAGNTGGNGCGCCCTTCCCATTTGCCTGTCCTGGTCAGGCCCCACCCCTTCCCACNTG
ACCAGCCATGGGGCTGCGGTGTTTTTCGGCTGCACTTTCGTGCGGTTGCGCCCGGCCTTCG
CGCTTTTCTTGATCACTGTGGCTGGGGACCGCTTCGCGTTATCATCCTGGTCGAGGGGCA
TTTTTCTGGCTGGTCTCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTTGGTCCATGTGAC
CGACCGGTCAGATGCCCGGCTCCAGTACGGCCTCCTGATTTTGGTGCTGCTGTCTGTCC
TTCTACAGGAGGTGTTCCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGTTA
GCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCTATGTTTCTGG
TCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTGGCTGATGCACTTG
GGCCAGGTGTGGTTGGGATCCATGGAGACTCACCC

FIGURE 224

GTAAAAGAAAGTGGCCGGACCTTCATTGGGGTTTCGGTTCCTCCCTTTCCCNNTCCCGGGG
TCTGGGGGTGACATTGCACCGCGCCCNCTCGTGGGGTCGCGTTGCCACCCACGCGGACTCCC
CAGNTGGCGCGCCCTCCCATTTGCCGTGTCCTGGTCAGGCCCCACCCCTTCCACCTGA
CCAGCCATGGGGGCTGCGGTGTTTTTCGGGCTGCACTTTCGTCGCGTTCGGGCCCCGGCCTTC
GCGCTTTTCTTGATCACTGTGGCTGGGGACCGCTTCGCGTTATCATCCTGGTCGAGGGGC
ATTTTTCTGGCTGGTCTCCCTGCTCCTGGCTCTGTGGTCTGGTTCATCTGGTCCATGTGA
CCGACCGGTGAGATGCCCGGCTCCAGTACGGCTCCTGATTTTTGGTGCTGCTGTCTCTGTC
CTTCTACAGGAGGTGTCCGCTTGCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGT
AGCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCTATGTTTCTG
GTCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTGGCTGATGCACTT
GGGCCAGGTGTGGTTGGGATCCATGGAGAC

000000-1101

FIGURE 225

GCCCCAGGGAGCAGTGGGTGGTTATAACTCAGGCCCGGTGCCAGAGCCCAGGAGGAGGCAG
 TGCCCAGGAAGGCACAGGCCCTGAGAACTCTGCGGCTGAGCTGGGAGCAAATCCCCACCCCC
 TACCTGGGGACAGGGCAAGTGAGACCTGGTGAGGGTGGCTCAGCAGGCAGGGGAGGAGAGG
 TGCTGTGCGCTCTGCACCCACATCTTTCTCTGTCCCTCCTTGCCCTGTCTGGAGGCTGCT
 AGACTCCTATCTTCTGAATTCTATAGTGCTGGGTCTCAGCGCAGTGCCGATGGTGGCCCCGT
 CCTTGTTGGTTCCCTCTCTACCTGGGGAATAAGGTGCAGCGGCC**AT**GGCTACAGCAAGACCCC
 CCTGGATGTGGGTGCTCTGTGCTCTGATCACAGCCTTGCTTCTGGGGGTACAGAGCATGTT
 CTCGCCAACAATGATGTTTCTGTGACCACCCCTCTAACACCGTGCCCTCTGGGAGCAACCA
 GGACCTGGGAGCTGGGGCCGGGAAGACGCCCGGTGGATGACAGCAGCAGCCGCATCATCA
 ATGGATCCGACTGCGATATGCACACCAGCCGTGGCAGGCCGCGCTGTTGCTAAGGCCAAC
 CAGCTCTACTGCGGGCGGTGTTGGTGATCCACAGTGGCTGCTCAGGCCGCCCACTGTCAG
 GAAGAAAGTTTTCAGAGTCCGTCTCGGCCACTACTCCCTGTCAACAGTTTATGAATCTGGGC
 AGCAGATGTTCCAGGGGGTCAAATCCATCCCCACCCCTGGCTACTCCACCCCTGGCCACTCT
 AACGACCTCATGCTCATCAAACCTGAACAGAAGAATTCGTCCCACTAAAGATGTCAGACCCAT
 CAACGCTCTCCTCTCATTTGTCCTCTGCTGGGACAAAGTGCTTGGTGCTGGCTGGGGACAA
 CCAAGAGCCCCCAAGTGCCTTCCCTAAGGTCTCCAGTGCTGAATATCAGCGTGCTAAGT
 CAGAAAAGGTGCGAGGATGCTTACCCGAGACAGATAGATGACACCATGTTCTGCGCGGTGA
 CAAAGCAGGTAGAGACTCTGCCAGGGTGATTCTGGGGGGCCTGTGGTCTGCAATGGCTCCC
 TGCAGGGACTCGTGTCTTGGGGAGATTACCCTTGTCGCCGGCCCAACAGACCGGGTGTCTAC
 ACGAACCTCTGCAAGTTCACCAAGTGGATCCAGGAAACCATCCAGGCCAACTCT**TGA**GTCTAT
 CCCAGGACTCAGCACACCGGCATCCCCACCTGCTGCAGGGACAGCCCTGACACTCCTTTCAG
 ACCCTCATTCCTTCCCAGAGATGTTGAGAATGTTTATCTCTCCAGCCCTGACCCCATGTCT
 CCTGGACTCAGGGTCTGCTTCCCCACATTGGGTGACCGTGTCTCTAGTTGAACCTGG
 GAACAATTTCCAAAAGTGTCCAGGGCGGGGTGCGTCTCAATCTCCCTGGGGCACTTTCAT
 CCTCAAGCTCAGGGCCCATCCCTTCTCTGCAGCTCTGACCCAAATTTAGTCCAGAAATAAA
 CTGAGAAGTGGAAAAAAA

FIGURE 226

MATARP P M W V L C A L I T A L L L G V T E H V L A N N D V S C D H P S N T V P S G S N Q D L G A G A G E D A R S D D
S S S R I I N G S D C D M H T Q P W Q A A L L L R P N Q L Y C G A V L V H P Q W L L T A A H C R K K V F R V R L G H Y S L S
P V Y E S G Q Q M F Q G V K S I P H P G Y S H P G H S N D L M L I K L N R R I R P T K D V R F I N V S S H C P S A G T K C L
V S G W G T T K S P Q V H F P K V L Q C L N I S V L S Q K R C E D A Y P R Q I D D T M F C A G D K A G R D S C Q G D S G G P
V V C N G S L Q G L V S W G D Y P C A R P N R P G V Y T N L C K F T K W I Q E T I Q A N S

FIGURE 227

ATGTGTCAAACGACCCGGTGGAAAGACCATGGGCGGGCTGCCAACTTGAGGACCGGCCCGCGCGA
 CAAGCCGACGCGGCCGAGCTGCGGCTACGTGCTGTGCACCGTGCTGCTGGCCCTGGGTGTGC
 TGCTGGCTGTAGCTGTGTACCCGGTGCCTGCTCTTCTGAACCAACCGCCACGCGCGGGCAGC
 GCGCCCCCACTGTGCTGAGCACTGGGGCTGCCAGCGCCAAAGCGCCCTGGTCACTGTGGGA
 AAGGGCGGACAGCTGCGACCTCAGCATCTATTGACCGGGCTGCCCGACCTCACCGACA
 GCTTCGCAAGCTGGAGAGCGCCAGGCCCTCGGTGCTGCAGGCGCTGACAGAGCACAGCGGCC
 CAGCCACGGCTGTGTGGGCAACAGGAGCAGGAGCTGCTGGACAGCTGCCGACCAAGCTGCC
 CCGGCTGTGCTGCCCGAGCCTCAGAGCTGCAGACGGAGTGCATGGGGCTGCGGAAGGGGCATG
 GCACGCTGGGCGAGGGCCTCAGCGCCCTGCAGAGTGAGCAGGGCGCGCTCATCCAGCTTCTC
 TCTGAGAGCCAGGGCCACATGGCTCACCTGGTGAACCTCCGTGAGGCACATCTGGATGCCCT
 GCAGAGGGACGGGGGCTGGGCCGGCCCGCAACAAGGCCGACCTTCAGAGAGCGCCTGCC
 GGGGAACCCCGGCCCGGGGCTGTGCCACTGGCTCCCGGCCCGAGACTGTCTGGACGTCTCT
 CTAAGCGGACAGCAGGACGATGGCGCTTACTCTTCTTCCACCCACTACCCGGCCGGCTT
 CCAGGTGTACTGTGACATGCGCAGGACGGCGCGGCTGGACGGTGTTCAGCGCCGGGAGG
 ACGGCTCCGTGAACCTTCTTCGGGGCTGGGACGCTACCGAGACGGCTTGGCAGGCTCAC
 GGGGAGCACCTGGCTAGGGCTCAAGAGGATCCACGCCCTGACCACACAGGCTGCTACGAGCT
 GCACGTGGACTTGAGGACTTTGAGAATGGCACGGCCTATGCCCGCTACGGGAGCTTCGGG
 TGGGCTTGTCTCCGTGGACCTTGAGGAAGACGGGTACCCGCTCACCGTGGCTGACTATTC
 GGCACTGCAGGCGACTCCCTCTGAAGCACAGCGGCATGAGGTTCAACCAAGGACCGTGA
 CAGCGACCATTCAGAGAAACACTGTGCGCCTTCTACCGCGGTGCTGGTGGTACCGCAACT
 GCCACAGCTCAACCTCAATGGGAGTACTGCGCGGTGCGCACGCCCTGCGCAGCGC
 GTGGAGTGGTCTCTTGACCGGCTGGCAGTACTCACTCAAGTTCTCTGAGATGAAGATCCG
 GCCGCTCCGGGAGGACCGCT**TAG**ACTGGTGCACCTTGCTTGGCCCTGGTGGTCCCTGTGCG
 CCATCCCGGACCCCACTCACTCTTTCTGTAATGTTCTCCACCCACTGTGGCTGGCGGAC
 CCACTCTCGATAGGAGGGGCGGGCCATCCCTGACACGAAGCTCCCTGGCCGGTGAAGT
 CACACATCGCTCTCGCCGCTCCCAACCCCTCCATTGGCAGCTCACTGATCTCTGCGCT
 TGCTGATGGGGGCTGGCAACTTGACGACCCCACTCTGCTGCCCGCACTGTGACTCGG
 TGCTGTTGGCTGCCCTGGCCAGGATGTGGAGTCTGCCCGAGGCACTCTGCGCTGCC
 GCGCAATACCCCGCAATTAGGGGACAGAGCAGGGGGCAGACAGACCCCTGGAGTCTCT
 CTAGCAGATCGTGGGGAATGTCAAGTCTCTCTGAGGTGAGGTCTGAGGCCAGTATCTCTCAG
 CCTCCCAATGCCAACCCCAACCCGTTTCCCTGGTGCCAGAGGACCCACTCTCCCCCA
 GGGCCTCAGCCTGGCTGTGGGCTGGGTGGCCCATCTTACAGGGCCTGAGGTGAGGATGGG
 GAGCTGCTGCTTTGGGGACCCAGCTCTCAAGGCTGAGACAGTTCCTTGGAGGCCACCCAC
 CCTGTGCCCGGCGAGGCTGGGGCTGCGAGTCTCTTACCTGCTGTGCCACCTGCTGCTG
 TCTCAATGAGGCCCAACCCATCCCCACCAAGCTCCCGGCTGCTCTACCTGGGCGAGC
 CGGGGCTGCCATCCATTCTCTGCTCTGGAAGGTGGGTGGGCGCTGACCGTGGGGCT
 GGACTGCGCTAATGGGAAGCTCTTGGTTTTCTGGGCTGGGGCCTAGGCAGGGCTGGGATGAG
 GCTTGTACAACCCCAACCAAAATTTCCAGGGAAGTCCAGGGTCTGAGGCTCCAGGAGG
 GCTTGGGGGTGATGACCCCTTCCCTGAGGTGCTGCTCATGAGGAGGCCAACCTTGGC
 ATTGACCGTGGCCACTGGACCCAGGCCAGGCCCGGCCCGCGAGTGGTCAAGGGACAGGGA
 CCACCTCAGCGGCAATGGGGTGGGGGACTGGGGCACAGGACAGGACCACTGAGTGA
 TCTTCTTGTGTAATCTCCCAACACCCAGCACGCTGTATCCCACTCTCTGTGTGACACA
 TTGAGAGGTGAGACCCGAGGCTCCAGGACAGGACAGGACAGGCGAGGCTGGAGCCGG
 TCTCTAGCTGTCTGCTCAGCAGCCTTGGACCCGCGTGCCTTACGCTAGGCCAGATGAGG
 CGGCTTTTCAAGGCCTCTGATGGGGGCTCGAAAGGCTGGAGTCAGCTTGGGGAGCT
 GCTAGCAGCTCTCTCTGGGCGAGGGGAGGTGGCTTCTCCAAAGGACACCCGATGGGA
 GTGCTCTAGGGGTGTGGGTTCCGTTCTCCCTCCCACTGAAGTTTGTGCTTAAAA
 AACAAATAAATTTGACTTGGCACCACTGGGGGTGGTGGGAGAGGCCGTGTGACCTGGCTCT
 TGTCAGAGTGCCACCAAGTTCATCCATGCGCAG

000000440
 11001

FIGURE 228

MVNDRWKTMGGAAQLED RPRDKPQRPS CGYVLCTVLLALAVLLAVAVTGAVLFLNH AHAPGT
APPPVVSTGAASANSALVTVERADSSHLSILIDPRCPDLTDS FARLESAQASVLQALTEHQA
QPRLVGDQE QELLDTLADQLPRLARASELQTECMGLRKHGTLGQGLSALQSEQGRLIQLL
SESQGHMAHLVNSVSDILDALQRDRGLGRPRNKADLQRAPARGTRPRGCATGSRPRDCLDVL
LSGQQDDGVYSVFPTHYPAGFQVYCDMRTDGGGWTVFQRRDGSVNFFRGWDAYRDGFGRLT
GEHWLGLKRIHALTTQAAYELHVDLED FENGTA YARYGSFGVGLFSVDPEEDGYPLTVADYS
GTAGDSLKHSGMRFTTKDRSDHSENNCAAFYRGAWWYRNCHTSNLNGQYLRGAHAS YADG
VEWSSWTGWQYSLKFSEMKIRPVREDR

FIGURE 229

GCAGTCAGAGACTTCCCCTGCCCTCGCTGGGAAAGAACATTAGGAATGCCTTTTAGTGCCT
 TGCTTCTCTGAAGTACAGTACAGTAGCCCGCGGCCAGGGCAATCCGACCACATTTACTCT
 CACCGCTGTAGGAATCCAGATGCAGGCCAAGTACAGCAGCAGAGGGACATGCTGGATGATG
 ATGGGGACACCACCATGAGCCTGCATTCTCAAGCCTCTGCCACAACCTCGGCATCCAGAGCCC
 CGCGGCACAGAGCACAGGGCTCCCTCTTCAACGTGGCGACCAGTGGCCCTGACCCCTGCTGAC
 TTTGTGCTTGGTGTCTGTATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTCAGTACTACC
 AGCTCTCCAATACTGGTCAAGACACCATTCTCAAATGGAAGAAAGATTAGGAAATACGTCC
 CAAGAGTTGCAATCTCTTCAAGTCCAGAATATAAAGCTTGCAGGAAGTCTGCAGCATGTGGC
 TGAAAAACTCTGTCTGAGCTGTATAACAAAGCTGGAGCACACAGGTGCAGCCCTTGTACAG
 AACAAATGAAATGGCATGGAGACAATTGCTACCAGTTCTATAAAGACAGCAAAAGTTGGGAG
 GACTGTAAATATTTCTGCCTTAGTGAAAACCTTACCATGCTGAAGATAAACAAACAAGAAGA
 CCTGGAAATTTGCCGCGTCTCAGAGCTACTCTGAGTTTTTCTACTCTTATTTGGACAGGGCTTT
 TGCGCCCTGACAGTGGCAAGGCCCTGGCTGTGGATGGATGGAACCCCTTTCACTTCTGAACGTG
 TTCCATATTATAATAGATGTCAACAGCCCAAGAAGCAGAGACTGTGTGGCCATCTCTCAATGG
 GATGATCTTCTCAAAGGACTGCAAAGAAATGAAGCGTTGTGTCTGTGAGAGAAGGGCAGGAA
 TGGTGAAGCCAGAGAGCCTCCATGTCCCCCTGAAACATTAGGCGAAGGTGACTGAATTCCGC
 CTCTGCAACTACAATAGCAGAGTGAGCCAGGCGGTGCCAAAGCAAGGGCTAGTTGAGACAT
 TGGGAAATGGAACATAATCAGGAAAGACTATCTCTCTGACTAGTACAAAATGGGTTCTCGTG
 TTTCTGTTCAGGATCACCAGCATTTCTGAGCTTGGGTTTATGCACGTATTTAACAGTACA
 AGAAGTCTTATTTACATGCCACCAACCAACCTCAGAAACCCATAATGTGCATCTGCCTTCTTG
 GCTTAGAGATAAATTTTAGCTCTCTTTCTCTCAATGTCTAATATCACCTCCCTGTTTTCAT
 GTCTTCCTTACACTTGGTGGAAATAAGAACTTTTGAAGTAGAGGAAATACATTGAGGTAAC
 ATCCTTTTCTCTGACAGTCAAGTAGTCCATCAGAAATGGCAGTCACTTCCCAGATTGTACC
 AGCAATACACAAGGAATCTTTTTGTTTGTTCAGTTCATACTAGTCCCTTCCCAATCCAT
 CAGTAAGAGCCCATCTGCCTTGTCCATGCCGTTTCCCAACAGGGATGTCACTTGATATGAG
 AATCTCAAATCTCAATGCCTTATAAGCATTCCTTCTGTGTCCATTAAAGACTCTGATAATTG
 TCTCCCTCCATAGGAATTTCTCCCAGGAAAGAAATATATCCCATCTCCGTTTCATATCAG
 AACTACCGTCCCCGATATTCCCTTCAGAGAGATTAAAGACCAGAAAAAGTGAGCCCTCTTCA
 TCTGCACCTGTAATAGTTTCAGTTCCATTTTCTTCCATTGACCCATATTTATACCTTTTACG
 GTACTGAAGATTTAATAATAATAAATGTAATACTGTGAAAAA

MQAKYSSTRDMLDDDDGDTTMSLSHSQASATTRHPEPRRTEHRAPSSSTRWPVALTLLTLCLVLL
IGLAALGLLFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNIKLAGSLQHVAEKLCRE
LYNKAGAHRCSPCTEQWKWHGDNCYQFYKDSKSWEDCKYFCLSENSTMLKINKQEDLEFAAS
QSYSEFFYFSYWTGLLRPDSKGAWLMDGTPFSTSELFHIIIDVTSRPSRDCVAILNGMIFSKD
CKSEKRCVCERRAGMVKFPELSHVPETLGGDD

FIGURE 231

AATTTTCACCGCTGTAGGAATCCAGATGCAGGCCAAGTACAGCAGCACGAGGGACATGNTGG
ATGATGATGGGACACCACCATGAGCCTGCATTNTCAAGCTTTTGCCACAATTCGGCATCCAG
AGCCCCGGCGCACAGAGCACAGGGNTCCTTTTTCAACGTGGCGACCAGTGGCCCTGACCCCTG
CTGACTTTGTGCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTCAGTA
CTACCAGCTCTCCAATACTGGTCAAGACACCATTCTCAAATGGAAGAAAGATTAGGAAATA
CGTCCCAAGAGTTGCAATTNTTCAAGTCCAGAATATAAAGCTTGCAGGAAGTNTGCAGCAT
GTGGCTGAAAAACTCTGTCGTGAGCTGTATAACAAAGCTGGAGGAACCTTGAAGGAGGGCAA
AGTNTCCTCATNTACTATACACACCACTTCCC

FIGURE 232

GCGGAGCGCAAGAACCCCTGCGCAGCCAGAGCAGCTGCTGGAGGGGAATCGAGGCGCGGCTC
 CGGGGATTTCGGCTCGGGCCGCTGGCTCTGCTCTGCGGGGAGGGAGCGGGCCCGCCCGCGGGT
 CCCGAGCCCTCCGGATCCGCCCCCTCCCGGTCGCCGCCCTCGGAGACTCTCTTGCTTGCTGCT
 CTGGGGGTTTCGCCGGGGCGGGGACCCCGCGGTCCGGGCGCC**atg**CGGGCATCGCTGCTGCTG
 TCGGTGCTCGGGCCCGCAGGGCCCGTGGCCGTGGGCATCTCCCTGGGCTTACCCCTGAGCCT
 GCTCAGCGCTACCTGGGTGGAGGAGCCGTGCGGCCACGGCCCGCCCAACCTGGAGACTCTG
 AGCTGCCCGCGCGCGGCAACACCAACGCGGCGCGCGCGGCCCAACTCGGTGCAGCCCGGAGCG
 GAGCGCGAGAAGCCCGGGGCGCGGAAGGCGCGGGGAGAATTGGGAGCCGCGGCTTTGCC
 CTACCACCTTGCACAGCCCGGCCAGGCCGCCAAAAAGGCCGTGAGACCCGCTACATCAGCA
 CGGAGCTGGGCATCAGGCAGAGGCTGCTGGTGGCGGTGCTGACCTCTCAGACCACGCTGCC
 ACGCTGGGCGTGGCCGTGAACCGCACGCTGGGGCACCGGCTGGAGCGTGTGGTGTCTCTGAC
 GGGCGCACGGGGCGCGCCGGGCCCACTGGCATGGCAGTGGTGACGCTGGGCGAGGAGCGAC
 CCATTGGACACCTGCACTGGCGCTGCGCCACCTGCTGGAGCAGCACGGCGACGACTTTGAC
 TGGTTCTTCTGTTGCTGACACCACTACACCGAGGCGCACGGCTGGCACGCCCTAACTGG
 CCACCTCAGCCTGGCCTCCGCGGCCCACTGTACCTGGGCGGGCCCAAGGACTTCATCGGGC
 GAGAGCCCAACCCCGCGCTACTGCCACGGAGGCTTTGGGGTGCTGCTGTGCGCATGCTGTG
 CTGACAACACTCGGCCCACTGGAAGGCTGCCGCAACGACATGCTCAGTGCGCGCCCTGA
 CGAGTGGCTGGGTGCTGCATTTCTCGATGCCACGGGGTGGGCTGCATGGTGACCACGAGG
 GGGTGCACTATAGGCATCTGGAGCTGAGCCCTGGGAGCCAGTGCAGAGGGGACCTCAT
 TTCCGAAGTGCCTTGACAGCCCAACCCCTGTGGCTGACCTGTGCACATGTACCAGCTGCACAA
 AGCTTTGCGCCGAGCTGAACCTGGAACGCACTGACAGGAGATCCAGGAGTTACAGTGGGAGA
 TCCAGAATACCCAGCATCTGGCCGTTGATGGGGACCGGCGAGCTGCTTGGCCCGTGGGTATT
 CCAGCACCATCCCGCCCGGCTCCCGCTTTGAGGTGCTGCGCTGGGACTACTTCACGGAGCA
 GCACGCTTTCTCCTGCGCCGATGGCTCACCCCGTGCCCACTGCGTGGGGCTGACCGGCTG
 ATGTGGCCGATGTTCTGGGGACAGCTCTAGAGGAGCTGAACCGCCGCTACCAACCCGGCCTTG
 CGGCTCCAGAAGCAGCAGCTGGTGAATGGTACCGACGCTTTGATCCGGCCCGGGGTATGGA
 ATACACGCTGGACTTGCAGCTGGAGGCACTGACCCCCCAGGGAGGCCGCGCGGCCCTCACTC
 GCGAGTGACGCTGCTCCGGCCGCTGAGCCGCTGGAGACTTTGCCGTGTGCCCTATGTCACT
 GAGGCCCTCAGCTCACTAGTGCTGTGCTCTAGCTGCGGCTGAGCGTGACCTGGCCCTGG
 CTTCTTGAGAGCCCTTTGCCACTGCAGCACTGGAGCCTGGTGATGCTGCGGCAGCCCTGACCC
 TGCTGCTACTGTATGAGCCGCGCCAGGCCAGCGCGTGGCCCATGCAGATGTCTTCGCACCT
 GTCAAGGCCACGTTGGCAGAGCTGGAGCGCGCTTCCCGGTGCGCGGTTGCCATGGCTCAG
 TGTGCAGACAGCCGACCTCACCACTGCGCCTCATGGATCTACTCTCCAAGAAGCACCCGCG
 TGGACACACTGTTCTGCTGGCGGGGCCAGACGGTGCTCAGCGCTGACTTCTTGAACCCGCG
 TGCCGCTGATGCATCTCCGCTGCGAGGCTTCTTTCCATGCAATTTCCAGACCTTTCA
 CCCAGGTGTGGCCCCACCACAAGGGCTTGGGCCCCAGAGCTGGGCGGTGACACTGGCCGCT
 TTGATCGCCAGGCGAGCCAGCGAGGCTGCTTCTACAACTCCGACTACGTGGCAGCCGTGGG
 CGCCTGGCGGCAGCCTCAGAACAAAGAAGAGGAGCTGCTGGAGAGCCTGGATGTGTACGAGCT
 GTTCTCTCACTTCTCCAGTCTGCATGTGCTGCGGGCGGTGGAGGCCGCGCTGCTGCAGCGCT
 ACCGGCTCAGCAGCTGCAGCGCAGGCTCAGTGAGGACCTGTACCCGCTGCCCTCCAGAGC
 GTGCTTGAGGGCCTCGGCTCCCGAACCCAGCTGGCCATGTACTCTTTGAACAGGAGCAGGG
 CAACAGCACT**TGA**CCCCACCTGTCCCGCTGGCGGCTGGCATGGCCACACCCCAACCCCACTT
 CTCCCCAAAACAGAGCCACCTGCCAGCCTCGCTGGGCGAGGCTGGCCGTAGCCAGACCCC
 AAGCTGGCCCACTGGTCCCTCTCTGGCTCTGTGGGTCCCTGGGCTGTGGACAGCAGCTGGG
 GGACGTGCCCCAGAGGCCACCCACTTCTCATCCAAACCCAGTTTCCCTGCCCTTGACGCT
 GCTGATTCCGGCTGTGGCCTCCACGATATTTATGCAGTACAGTCTGCTGACGCCAGCCCTGC
 CTCTGGGCCCTGGGGCTGGGCTGTAGAAGAGTTGTTGGGGAAGGAGGAGCTGAGAGGGG
 GCATCTCCCAACTTCTCCCTTTTGACCCCTGCCGAAGCTCCCTGCCTTTAATAAACTGGCCA
 AGTGTGAAAAA

MRASLLLSVLRPAGPVAVGISLGFTLSLLSVTWVEEPCGPGPPQPGDSELPPRGNTNAARRP
NSVQPGAEREKPGAGEGAGENWEPRVLPYPHPAQPGQAAKAVRTRYISTELGIRQRLVAVL
TSQTTLPTLGVAVNRNLGHRLERVVFLTGARRRAPPGMAVVTLGEERPIGHLHLALRHLE
QHGDDEFDWFLLVPDTTYTEAHLARLTGHLSLASAAHLYLGRPDFIGGEPTPGRYCHGFGF
VLLSRMLLQQLRPHLEGCNRNDIVSARPDWLGRCILLDATGVGCTGDHEGVHYSHLELSPGEP
VQEGDPHFRSALTAPHVPRDPVHMYQLHKAFARAELEPTYQEIQELQWEIQNTSHLAVDGDRA
AAWPVGI PAPS RPAS RFVL RWDY FTEQHAFSCADGSPRCPLRGADRADVADVLGTALAEELN
RRYHPALRLQKQQLVNGYRRFDPARGMEYTLDLQLEALTPQGRRPLTRRVQLLRPLSRVEI
LPVPYVTEASRLTVLLPLAAERDLAPGFLEAFATALEPGDAAAALTLLLYEPRQAQRVA
HADVFAPVKAHVAELERRFPGARVPWLSVQTAAPSPRLRMDLLSKKHPLDTLFLLAGPDTVL
TPDFLNRCRMHAISGWQAFFPMHFQAFHGPVAPPQGPPELGRDTRGRDQAASEACFYNS
DYVAARGRLAAASEQEELLESLDVYELFLHFSSLHVRAVEPALLQRYRAQTCARSLEDL
YHRCLOSLVLEGLGSRQTOLAMLLFEQEQGNST

GCTCTGGCCGGCCCCGGCGATTGGTCACCGCCGCTAGGGGACAGCCCTGGCCTCCTCTGAT
TGGCAAGCGCTGGCCACCTCCCCACACCCTTGCGAACGCTCCCTAGTGGAGAAAAGGAGT
AGCTATTAGCCAATTTCGGCAGGGCCCGCTTTTTAGAACTTGATTTCCTTTGAAGATGAAAG
ACTAGCGGAAGCTCTGCCTCTTTCCCACTGGGCGAGGGAACCTCGGGCGATTGGCTGGGAA
CTGTATCCACCCAATGTCACCGATTCTTCTCTATGACAGGAAATGAGCAGACCCATCAATAA
GAAATTTCTCAGCCTGGCCGAAAATGGTTGGCCCCACGAAGCCACGACAACCTGGAGGGCAAAG
AGGGTTGCTCAACGCCCCGCCTCATTTGGAAGAACCAATCAGATCTGGGACCTATATAGCGTG
GCGGAGGCGGGGCGATGATTGTCGCGCTCGCACCCACTGCAGCTGCGCACAGTCGCATTTCT
TTCCCCGCCCTGAGACCCTGCAGCACCATCTGTCA**ATG**CGCGCTGGGCTGTTTGGTTTGAGC
GCTCGCCGTCTTTTGGCGGCAGCGCGCGACGCGAGGGCTCCCGGCCGCCCGCGTCCGCTGGGA
ATCTAGCTTCTCCAGGACTGTGGTCGCCCGTCCGCTGTGGCGGGAAAGCGGCCCCAGAAC
CGACCACACCGTGGCAAGAGGACCCAGAACCAGGAGACGAAAACCTGTATGAGAAGAACCCA
GACTCCCATGGTTATGACAAGGACCCCGTTTTGGACGCTCTGGAACATGCGACTTGTCCTTCT
CTTTGGCGTCTCCATCATCTTGGTCCTTGGCAGAGCCCTTGTGGCCATATGCTCGCTGACTACA
GGATGAAAGATGGTCCCGCCGCGAAGCTGAGAGGCTTGTGAATACCGAGAGGCCAATGGC
CTTCCCATCATGGAATCCAACTGACTTTCGACCCGACCAAGATCAGCTGCCAGAGGATGAGT**G**
ACCAGTTGCTAAGTGGGGCTCAAGAAGCACCGCCTTCCCCACCCCTGCCTGCCATTCTGAC
CTCTTCTCAGAGCACCTAATTAAGGGGCTGAAAGTCTGAA

FIGURE 236

GGCGGCTGGGCTGTTTGGTTTGAGCGCTCGCCGTCTTTTGGCGGCAGCGGCGACGCGAGGGC
TCCCGGCCGCCGCGCTCCGCTGGGAATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCGCT
GTGGCGGGAAGCGGCCCCAGAACCGACCACACCGTGGCAAGAGGACCCAGAACCCGAGGA
CGAAAACTTGTATGAGAAGAACCAGACTCCCATGGTTATGACAAGGACCCGTTTTGGACG
TCTGGAACATGCGACTTGTCTTCTTTGGCGTCTCCATCATCCTGGTCCTTGGCAGCACC
TTTGTGGCCTATCTGCCTGACTACAGGATGAAAGAGTGGTCCCGCCGCGAAGCTGAGAGGCT
TGTGAAATACCGAGAGGCCAATGGCCTTCCCATCATGGAATCCAAGTCTCGACCCAGCA
AGATCCAG

FIGURE 237

GCGCGCGCTATGCGGCTTGCTCTGCTCGTCTGTGCTCTCTGGGCGCGCGGCTGGTGCCT
 TGCAGAACCCCCACGCGACAGCCTGCGGGAGGAACTGTGCATACCCCCGCTGCCTTCCGGGG
 ACGTAGCCCGCACATTCCAGTTCCGACGCGCTGGGATTTCGAGCTTCAGCGGGAAGGAGTG
 TCCCATTACAGGCTCTTTCCCAAAGCCCTGGGGCAGCTGATCTCCAAGTATTCTCTACGGGA
 GCTGCACCTGTCACTTACACAAGGCTTTTGGAGGACCGGATCTGCGGGCCACCTTCCTGC
 AGGCCCCATCAGGTGCAGAGCTGTGGGTCTGGTTCCAAGACACTGTCACTGATGTGGATAAA
 TCTTGGAAGGAGCTCAGTAATGTCTCTCAGGGATCTTCTGCGCCTCTCTCAACTTCATCGA
 CTCCACCAACACAGTCACTCCCACTGCCTCCTTCAAACCCCTGGGTCTGGCCAATGACACTG
 ACCACTACTTTCTGCGCTATGCTGTGCTGCCGCGGAGGTGGTCTGCACCGAAAACCTCACC
 CCTTGAAGAAGCTCTTGCCCTGTAGTTCCAAGGCAGGCTCTCTGTGCTGCTGAAGGCAGA
 TCCTTGTGTTCCACACAGCTACCACTCCCAAGGCAGTGATATCCGCCCCGTTTTCAGAAAATG
 CACGCTGTACTAGCATCTCTGGGAGCTGAGGCAGACCCTGTCACTTGTATTGTATGTCCTTC
 ATCAGGGGCGAGGAAAAGAAAGACTGGTCCCTCTTCCGGATGTTCTCCCGAACCTCACGGA
 GCCCTGCCCCCTGGCTTCAGAGAGCCGAGTCTATGTGGACATCACCACCTACAACACAGGACA
 ACGAGACATTAGAGGTGACCCACCCCGACCACTACATATCAGGACGTCATCTTAGGCACT
 CGGAAGACCTATGCCATCTATGACTTGCTTGACACCGCCATGATCAACAACCTCTCGAAACCT
 CAACATCCAGCTCAAGTGAAGAGACCCCAAGAAATGAGGCCCCCCAGTGCCTTCCTGC
 ATGCCAGCGGTACGTGAGTGGCTATGGGCTGCAGAAGGGGAGCTGAGCACACTGCTGTAC
 AACACCCACCCATACCGGGCTTCCCGGTGCTGCTGCTGGACACCGTACCCTGGTATCTGGG
 GCTGTATGTGCACACCTCACCATCACCTCCAAGGGCAAGGAGAACAAACCAAGTTACATCC
 ACTACCAGCCTGCCAGGACCGGCTGCAACCCCACTCCTGGAGATGCTGATTGAGTGCCTG
 GCCAACTCAGTCACCAAGGTTTCCATCCAGTTTGAAGGGGCGCTGCTGAAGTGGACCGAGTA
 CAGCCAGATCTTAACCATGGCTTCTATGTCAGCCCATCTGTCTCAGCGCCCTTGTGCCCA
 GCATGGTAGCAGCAAGCCAGTGGACTGGGAAGAGATCCCTCTTCAACAGCCTGTTCCCA
 GTCTCTGATGGCTCTAACTACTTTGTGCGGCTCTACACGGAGCCGCTGCTGGTGAACCTGCC
 GACACCGGACTTCAGCATGCCCTACAACGTGATCTGCCTCACGTGCACCTGGTGGCCGTGT
 GCTACGGCTCCTTACAACTCTCTCACC CGAACCTTCCACATCGAGGAGCCCCGACAGGT
 GGCTTGGCCAAGCGCTGGCCAACCTTATCCGCGCGCCCCGAGGTGTCCCCCACTCTGAATT
 CTGCGCTTTCCAGAGCTGCAGCTGCCGTTTCTCTGCGGGAGGGGAGCCCAAGGCTGTT
 TCTGCCACTTGCTCTCTCAGAGTTGGCTTTTGAACCAAAGTGCCCTGGACAGGTACAGGC
 CTACAGCTGTGTTGTCCAGTACAGGAGCCACGAGCCAAATGTGGCAATTTGAATTTGAATTA
 CTTAGAAATTCATTCTCCACCTGTAGTGCCACCTCTATATTGAGGTGCTCAATAGCAAA
 AGTGTGCGGTGGCTGCTGTATTGGACAGCACAGAAAAAGATTTCCATCACCACAGAAGGTC
 GGCTGGCAGCACTGGCCAAGGTGATGGGCTGTGCTACACAGTGTATGTCACTGTGTAGTGA
 TGGAGTTTACTGTTGTGGAATAAAAACGGCTGTTTCCGTGGAAAAA

TGAATT "04h06660

FIGURE 238

MPLALLVLLLLGPGGWCLAEPPRDSLREELVITPLPSGDVAATFQFRTRWDELQREGVSHY
RLFPKALGQLISKYSLRELHLSFTQGFWRTYWGPPFLQAPSGAELWVWFQDVTVDVDSWK
ELSNVLSGIFCASLNFIDSTNTVTPTASFVKPLGLANDTDHYFLRYAVLPREVVCTENLTPWK
KLLPCSSKAGLSVLLKADRLFHTSYHSQAVHIRPVCRNARCTSSISWELRQTLSSVFDAFITG
QGKKDWSLFRMFSRTLTEPCPLASESRVYVDITTYNQDNETLEVHPPPTTTYQDVILGTRKT
YAIYDLLDTAMINNSRNLNIQLKWKRPENEAPPVPFLHAQRYVSGYGLQKGELSTLLYNTH
PYRAFPVLLLDTPVWYLRLYVHTLTITSKGKENKPSYIHYQPAQDRQLPHLLEMLIQLPANS
VTKVSIOFERALLKWTEYTPDPNHGFYVSPSVLSALVPSMVAAPVDWEESPLFNSLFPVSD
GSNYFVRLYTEPLLNLPTPDFSMPYNVICLTCTVVAVCYGSFYNLLTRTFHIEEPTGGLA
KRLANLIRRARGVPPL

CAACATG GGGTCCAGCAGCTTCTTGGTCCTCATGGTGTCTCTCGTTCTTGTGACCTGTGTG
CTGTGGAAGGAGTTAAAGAGGGTATAGAGAAAGCAGGGGTTTGCCACAGTGACAACGTACGC
TGCTTCAAGTCCGATCCTCCCAAGTGTCACACAGACCAGGACTGTCTGGGGGAAAGGAAGTG
TTGTTACCTGCACTGTGGCTTCAAGTGTGTGATTCTGTGAAGGAAGTGGAGAAGGAGAGAA
ACAAGGATGAAGATGTGTCAAGGCCATACCTGAGCCAGGATGGGAGGCCAAGTGTCCAGGC
TCCCTCTCTACCAGGTGTCTCAGAAATGATGCTGGGTCTTTCTACCTCTGGGGGTCACTC
TCACTTGGCACCTGCCCTTGAGGGTCTTGAGACTTGGAATATGGAAGAAGCAATACCCAAAC
CCACCAAAGAAAACCTGAGCTTGAAGTCTTTTCCCCAAAAGAGGGGAAGAGTCACAAAAAG
TCCAGACCCAGGGACGGTACTTCCCTCTCTACCTGGTGTCTCTCCTAATGCTCATGAAT
GGACCCCTCATGAATGAACCAGTGCCCTTATAAGAGACCCCAAAGAGTGCCTTGCCCTT
TGCAATGTGTGATCAGAGCTAGAAGGCAGTGTGAGAGAAGAGAACTGGTCTCACCAGATG
CTGAATCTGTGATGCTCTTGTATCTTGGACTTCCAGCCTCTAGAAGTGTGAAGAAATAAATAT
TTGCTGTTTATAATCCAA

FIGURE 240

MGSSSFVLVLMVSLVLVTLVAVEGVKEGIEKAGVCPADNVRCFKSDPPQCHTDQDCLGERKCC
YLHCGFKCVIPVKELEEGGNKDEDVSRPYPEPGWEAKCPGSSSTRCPQK

Signal sequence:

amino acids 1-19

N-myristoylation sites:

amino acids 23-29, 27-33, 32-38, 102-108

WAP-type 'four-disulfide core' domain signature:

amino acids 49-63

FIGURE 241

AAACCTCAGCACTTGCCGGAGTGGCTCATTGTTAAGACAAAGGGTGTGCACCTTCTGGCCAGG
 AAACCTGAGCGGTGAGACTCCAGCTGCCTACATCAAGGCCCCAGGACATGCAGAACCTTCC
 TCTAGAACCAGCCACCCACCA**ATG**AGGTCCTGCCTGTGGAGATGCAGGCACCTGAGCCAAAGG
 CGTCCAGTGGTCTGTGCTTCTGGCTGTCTGGTCTTCTTCTTCTCGCCTTGCCCTCTTTTA
 TTAAGGAGCCTCAACAAAGCCTTCCAGGCATCAACGCACAGAGAACATTAAAGAAAGGTC
 CTACAGTCCCTGGCAAAGCCTAAGTCCCAGGCACCCACAAGGGCGAGGAGGACAACCATCTA
 TGCAGAGCCAGCGCCAGAGAACATGCCCTCAACACACAAACCCAGCCCAAGGCCACACCA
 CCGGAGACAGAGGAAAGGAGGCCAACAGGCACCGCCGAGGAGCAGGACAAGGTGCCCCAC
 ACAGCACAGAGGGCAGCATGGAAGAGCCAGAAAAAGAGAAAACCATGGTGAACACACTGTC
 ACCCAGAGGGCAAGATGCAGGGATGGCCTCTGGCAGGACAGAGGCACAATCATGGAAGAGCC
 AGGACACAAGAGCAGCCCAAGGAAATGGGGGCCAGACCAGGAAGCTGACGGCCTCCAGGAGC
 GTGTCAAGAGAAGCACAGGGCAAAGCGGCAACACAGCCAAAGACGCTCATTCCTCCAAAAGTCA
 GCACAGAATGCTGGCTCCACAGGAGCAGTGTCAACAAGGACGAGACAGAAAGGAGTGACCA
 CAGCAGTCATCCCACCTAAGGAGAAGAAACCTCAGGCCACCCACCCCTGCCCCCTTCCAG
 AGCCCCACGACGACAGAGAAACCAAAGACTGAAGGCCGCCAACTTCAAACTCTGAGCCTCGGTG
 GGATTTTGAGGAAAAATACAGCTTCGAAATAGAGGGCCTTCAGACGACTTGCCCTGACTCTG
 TGAAGATCAAGCCTCCAAGTCGCTGTGGCTCCAGAACTCTTCTGCCAACCTCACTCTC
 TTCTGGACTCCAGACACTTCAACCAGAGTGAGTGGGACCGCCTGGAACACTTTGCACCACC
 CTTTGGCTTCATGGAGCTCAACTACTCCTTGGTGCAGAAAGTCTGTGACACGCTTCCCTCCAG
 TGCCCCAGCAGCAGCTGCTCCTTGGCCAGCCTCCCGCTGGGAGCCTCCGGTGCACTCACCTGT
 GCCGTGGTGGCAACCGGGGCATCCTGAACAACCTCCACATGGGGCCAGGAGATAGACAGTCA
 CGACTACGTGTTCCGATTGAGCGGAGCTCTCATTAAAGGCTACGAACAGGATGTGGGACTC
 GGACATCCCTTACGGCTTTACCGCCTTCTCCCTGACCCAGTCACTCCTATATTGGGCCAAT
 CGGGGTTTCAAGAACGTGCCCTTGGGAAGGACGTCCGCTACTTGCACTTCTTGGGAAGGCAC
 CCGGGACTATGAGTGGCTGGGAAGCACTGCTTATGAATCAGACGGTGATGTCAAAAAACCTTT
 TCTGTTTCAGGCACAGACCCAGGAAGCTTTTCGGGAAGCCCTGCACATGGACAGGTACCTG
 TTGCTGCACCAGACTTTCTCCGATACATGAAGAACAGGTTTCTGAGGTCTAAGACCCCTGGA
 TGGTGCCCACTGGAGGATATACCGCCCCACCACTGGGGCCCTCCTGTGCTCACTGCCCTTC
 AGCTCTGTGACCAGGTGAGTGCTTATGGCTTCATCACTGAGGGCCATGAGCGCTTTTCTGAT
 CACTACTATGATACATCATGGAAGCGGCTGATCTTTTACATAAACCATGACTTCAAGCTGGA
 GAGAGAAGTCTGGAAGCGGCTACACGATGAAGGAGATAATCCGGCTGTACCCAGGCTCCTGGTC
 CGGAACTGCCAAGGCCAAGAACT**TGA**CGGGGCCAGGGCTGCCATGGTCTCCTTGGCTGCTC
 CAAGGCACAGGATACAGTGGGAATCTTGAGACTCTTTGGCCATCTTCCATGGCTCAGCTAA
 GCTCCAAGCCCTTCAAGGAGTTCCAAGGGAACACTTGAACCATGGACAAGACTCTCTCAAGAT
 GGCAATGGCTAAATTGAGTTCTGAAGTTCTTCAGTACATTGCTGTAGGTCTGAGGCCAGG
 GATTTTTTAATTAATGGGGTGATGGGTGGCCAAATACCACAATTCCTGCTGAAAAACACTCTT
 CCAGTCCAAAGCTTCTTGATACAGAAAAAGAGCCTGGATTACAGAAACATATAGATCTG
 GTTTGAATTCCAGATCGAGTTTACAGTTGTGAAATCTTGAAGGTATTACTTACTTCACTAC
 AGATTGCTAGAAAGACTTTCTAGGAGTTATCTGATTTAGAAAGGCTCTACTTGTCTCTG
 TCTTTAAGCTATTGACAACCTCTACGTGTTGTAGAAAACCTGATAATAATACAAATGATTGTT
 GTCCATGGAAGGCCAAATAAATTTTCTACAGTGAIAAAAAAAAAAAAAA

FIGURE 242

MRSCLWRCRHL SQGVQWSLL LVLVFFLFALPSFIKEPQTKPSRHQRTENIKERSLQSLAKP
 KSQAPTRARRTTIYAEPA PENNALNTQTQPKAHTTGDRGKEANQAPPEEQDKVPHTAQRAAW
 KSPEKEKTMVNTLS PRGQDAGMASGRTEAQSWKSQDTKTTQGNNGQTRKLTASRTVSEKHQG
 KAATAKTILIPKSQHRMLAPTGA VSTRTRQKGVT TAVIPPEKEKKQATPPPAFFQSPTTQRN
 QRLKAANFKSEPRWDFEEKYSFEIGGLQTTCPDSVKIKASKSLWLQKLFPLNLTFLDSRHF
 NQSEWDRLEHFAPPFGFMELNYSLVQKVVTFRFPVPVQQQLLASLPAGSLRCITCAVVGNGG
 ILNNSHMQEIDSHDYVFRLSGALIKGYEQDVGTRTSFYGF TAFSLTQSL LILGNRGFKNVP
 LGKDVRYLHFLEGRDYEWLEALLMNQTVMSKNLFWFRHRPQEA FREALHMDRYLLHPDFL
 RYMKNRFLRSKTL DGAHWRIYRPTTGALLLTALQLCDQVSAYGFITEGHERFSDHYDTSW
 KRLIFYINHDFKLEREVWKRLHDEGIIRLYQRPGPGTAKAKN

Cytoplasmic Domain:

amino acids 1-10

Type II Transmembrane Domain:

amino acids 11-35

Luminal catalytic Domain:

amino acids 36-600

Ribonucleotide Reductase small subunit Signature:

amino acids 481-496

N-glycosylation Sites:

amino acids 300-303, 311-314, 331-334, 375-378, 460-463

FIGURE 243

CCATGCGCGGACCCGGGCACCCCTCCTCCTGGGGCTGCTGCTGGTGCTGGGGCCTTCGCCG
GAGCAGCGAGTGGAATTGTTCCCTCGAGATCTGAGGATGAAGACAAGTTTCTAAAAACACCT
TACAGGCCCTCTTTATTTTAGTCCAAAGTGCAGCAAACACTTCCATAGACTTTATCACAACA
CCAGAGACTGCACCATTCTGCATACTATAAAAGATGCGCCAGGCTTCTTACCCGGCTGGCT
GTCAGTCCAGTGTGCATGGAGGATAAGTGAGCAGACCGTACAGGAGCAGCACACCAGGAGCC
ATGAGAAGTGCCTTGGAACCAACAGGGAAACAGAACTATCTTTATACACATCCCCTCATGG
ACAAGAGATTTATTTTGCAGACAGACTCTCCATAAGTCCTTTGAGTTTGTATGTTGTTG
ACAGTTTGCAGATATATATTCGATAAATCAGTGTACTTGACAGTGTTATCTGTCACTTATTT

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FIGURE 244

MRGPGHPLLGLLLVLGFSPEQRVEIVPRDLRMKDKFLKHLTGPLYFSPKCSKHFRLYHNT
RDCTIPAYYKRCARLLTRLAVSPVCMDK

000000-111111-000000

GGGCTGGGCCCGCCGCGAGCTCCAGCTGGCCGGCTTGGTCTCGGGTCCCTTCTCTGGGAGG
CCCCAGCCCGCGCGCGCCAGCCCCACCATGCCACCCGCGGGGCTCCGCGGGCGCGCCG
CTCACCGCAATCGCTCTGTTGGTGTCTGGGGGCTCCCCTGGTGTCTGGCCGGCAGGACTGCCT
GTGGTACCTGGACCGGAATGGCTCCTGGCATCCGGGGTTAACTGCGAGTTCTTCACCTTC
GCTGCGGGACCTGCTACCATCGGTACTGTCTGAGGGACCTGACCTTGCTTATCACCAGAGG
CAGCAGAAGCACTGCCTGGCCTTCAGCCCCAAGACCATAGCAGGCATCGCCTCAGCTGTGAT
CCTCTTTGTTGCTGTGGTTGCCACCACCATCTGCTGCTTCCTCTGTTCTCTGTGTACCTGT
ACCGCCGGCGCCAGCAGCTCCAGAGCCCAATTGAGGGCCAGGAGATTCCAATGACAGGCATC
CCAGTGCAGCCAGTATACCCATACCCCCAGGACCCCAAAGCTGGCCCTGCACCCCCACAGCC
TGGCTTACGTAGCCACCTAGTGGTCTGCTCCCAATATCCACTCTACCCAGCTGGGCCCC
CAGTCTACAACCTGCGAGCTCCTCCTCCCTATATGCCACCACAGCCCTCTTACCCGGGAGCC
TGAGGAACACAGCCATGTCTCTGCTGCCCCCTTCAGTGATGCCAACCTTGGGAGATGCCCTCAT
CCTGTACCTGCATCTGGTCTCGGGGTGGCAGGAGTCTCCAGCCACCAGGCCCCAGACCAA
GCCAAGCCCTGGGCCCTACTGGGGACAGAGCCCCAGGGAAGTGAACAGGAGCTGAACTAGA
ACTATGAGGGGTGGGGGGAGGGCTTGAATTATGGGCTATTTTTACTGGGGCAAGGGAGG
GAGATGACAGCCTGGGTACAGTGCTCTGTTTCAAATAGTCCCTCTGCTCCCAAGATCCAG
CCAGGAAGGCTGGGGCCCTACTGTTTGTCCCCTCTGGGCTGGGGTGGGGGAGGGAGGAGGT
TCCGTCAGCAGCTGGCAGTAGCCCTCCTCTGGCTGCCCATGGCCACATCTCTGGCCTG
CTAGATTAAAGCTGTAAGACAAA

FIGURE 246

MPPAGLRRRAAPLTAIALLLVLGAPLVLAGEDCLWYLDNRNGSWHPGFNCEFFTFCCGTCYHRYC
CRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVVATTICCFLCSCCYLYRRRQQLQSP
FEGQEIPMTGIPVQPVYPYPQDPKAGPAPPQPGFMYPPSGPAPQYPLYPAGPPVYNPAAPPP
YMPPQPSYPGA

Transmembrane Domains:

amino acids 10-28, 85-110

N-glycosylation Site:

amino acids 38-41

N-myristoylation Sites:

amino acids 5-10, 88-93

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GGGGGAGC TAGGCCGGCGGCAGTGGTGGTGGGGCGGCGCAAGGGTAGGGCGGCCAGAA
 CCCCAGGAGGTTAGTAGCAAGAAAGATGGTGTGTTCTGCCCCCTCAATGGTCCCTGCAACCATG
 TCAPTTCTACTTTCTCCACTGTGGCTCTCTTAACCTGTGTCACACTCTTCTATGGTGTCTAGC
 CACTGAAGCACTTCCAAAACGTGATGATGGGACCACTTTCTTGGATAAAATACGACTTC
 CTGATACGTGTCATCCCAAGTCTATTATGATCTCTGTATCATGCAAACTTACACGCTGACC
 TTTCTGGGGAACCCAGGAAGTAGAAATACAGCCGACTCAGCCACCAGCCACCATCATCTGCA
 TAGTCAACCACTGCGATATCTTAGGCCACCTCAGGAAGGGAGCTGGAGAGAGGCGTATGCG
 AAGAACAACCTGCAAGTCTTGGAAACACCCCTCAGGAGCAAAATGCACTGCTTGGCTCTCGGA
 CCCCCTCTGTCTGGGGCTCCCGGTACACAGTGTGTCATCTACTGTGSCAATCTCTGCGAAT
 TTTTCCACGGATTTTCAAAAAGCACTTACAGAACCAAGGAAGGGGAATCAGGAATCTGCTT
 CAACACAATTTGAACCACTGCGAGTAGAATGGCTTTTCCCTTTGATGAGTGTGCTT
 AAAGCAAGTTTCTCAATCAAAATTAGAAGAGGCGCAAGGCACCTAGGCTTCTGCAATATGCT
 ATTTGGTGAATCTGTGACTGTGCTGAAGGACATCAGGAAGACCACTTTGATGTCACTGTGA
 AGATGAGCAACCTATCTGGTGGCTCTCATCATTTAGATTTTGAAGCTGACACAGATAAAC
 AAGAGTGGAGTCAAGGTTTCTGTTTATGCTGCGACAGACAAGATAAATCAAGCAAGATTATG
 ACTGGATGCTCGGGTGACTCTCTAGAATTTAGAGATATTTCTCAGCATACCGTATCCCTT
 TACCCAAACAAAGATTTGCTGCTGCTGAGCTTATGATGCTGTGATGGAAACTGGGGA
 CTGACAACATATAGAGAATCTGCTCTGTTGTTGATGCAAGAAGTCTTCTGCATCAAGTAA
 GCTTGGCATCAGAGTCACTGTGGCCCATGAAGTGGCCACCACTGTTTGGGAACCTGTGTCA
 CTATGGAGTCAAGGAATGATCTTTGGCTAAATGAGATTTTGGCAAAATTTGAGCTTTGTG
 TCTGTCTGTGTCACCATTTGAACCTCAAAATGAGATTTATTTCTTTGGCAAAATTTTGA
 CGCAATGGAGGTAGATGCTTTAAATCTTCAACACTCTGTGCTTACCTGTGGAAATCTTGA
 CTCAGATCGGGGAGATGTTGAGATGTTTCTTATGATAAGGAGCTTGATTTCTGAAATG
 CTAAGGGAGATCTACGCTGTGACGCAATTTAAACTGTGATGTACAGTATCTCAGAACGCA
 TAGCTATAAAAAATATCAAAAGAGCACTGTGGATAGTATGGCAAGTATTTGCCCTACAG
 TGGTATATATAGGATGATGAGTCTTTTGTCTAGAACTCAACATCTATCTTCACTTCACAT
 TCTGCTATAGGAAGGGTGGATGTGAAACCAATGATGACACTTGGACACTCAGAGGGGTTT
 CCGCTCAATATATACAGTCAAGGGGAGGAATCTACACATGAAGCAAGACGACTACATGA
 AGGCTCTGACGCGCCGCCCGGACACTGGGTACCTGTGGCATGTTCCTATGACATTCATACC
 ACCAAATCAAACTGGTCCATCGATTTTGTCAAAAACAAAACAGATGTGCTCATCTTCCC
 AGAAGAGTGGAAATGGATCAAAATTAATGTGGGCATGAATGGCTATTACATTTGTCAATTAG
 AGGATGATGGATGGGACTTTTTCAGTGGCCTTTTAAAGGAACACACACAGCATCAGCAT
 AATGATCGGGCAAGTCTCATTAACAATGCATTTCAAGCTCGTCAGCATTTGGGAAGCTGTCCAT
 TGAAGAAGCCTTGATTTTATCTCCTGTACTTTGAACACTGAAACTGAAATATGCGCGTGTTC
 AAGTTTGAATGAGCTGATCTCATGTATGTAATGTTAAGTGAGAAAGAGATATGAATGAAGT
 GAAACTCAATTCAGGCCCTTCTCATGAGCTGCTAAGGACCTCATTTGATGAAGACAGATG
 GACAGCAGAGGGCTCAGTCTCAGAGCAAACTGCTCGGGTAGACTACTCTCTCGCCTGTG
 TGCACAACTCATCAGCGTGGCTGACAGAGGCGAAGGCTATTTAGAAAGTGGGAAGGAAATCC
 AATGGAACTTTGAGCTCGCTGTCGACGTACCTTGGCAGTGTGCTGTGGGGGCCCGAG
 CACAGAAGCTGGGATTTCTTTATAGTAATATCAGTTTCTTTGTCAGATCTGAGAAA
 GCGAAATGAATTTGCCCTCTGCAAGACCCCAAAATGAAGAAAAGCTTCAATGGCTACTAGAT
 GAAAGCTTTAAGGAGATAAAATAAAACCTCAGAGTTTCCACAAATCTTTACACTCATTTGG
 CAGGAACCCAGTAGGATGATCCACTCGGCTGGCAATTTCTGAGGAAAACCTGGAACCAACTGG
 TACAAAAGTTTGAACTTGGCTCATCTTCTCATAGCCACATGTTAATGGGTACACAACTCAA
 TTCTCAGCAAGAAACCGGCTTGAAGAGGTAAAGGATTTCTCAGCTCTTGAAGAAAATTTGG
 TTCTCAGTCCGTTGTGTCTCAACAGCAATTTGAACCAATTTGAGGAAAACCTCGGTTGGATGG
 ATAGAAGATTTGTATAAAATCAGAGTGTGGCTGCAAAAGTGAAAGCTTTGAACGTATGTAAAAA
 TTCTCCCTTCTCGCGGTTCTGTATCTCTAATCAACCAACTTTTGTGTAGTGTATTTTCAA
 ACTAGAGATGGCTGTGTTGGCTCCCACTGGAGATCACTTTTCCCTTCAACTCATTTTGTGA
 CTATCCCTGTGAAAAGAAATAGCTGTTAGTTTTCATGAATGGGCTTTTCTATGAATGGGCTA
 TCGCTACCATGTGTTTGTGTTTATCATCAGGTTGTGGCCTGCAAGCTAAACCCAGTGTGGGT
 TCCCTGCCACAGAAATAAATGATACCTTTATTTCTTCAAAAAAAAAAAAAAAAAAAAAAAA

MVFLPLKWSLATMSFLLSSLLALLTVSTPSWCQSTEASPKRSDGTPFPWNKIRLPEYIVPVH
YDLLIHANLTTLTFWGTTKVEITASQPTSTIILHSHHLQISRATLRKGAGERLSEEPQLQVLE
HPPQEQIALLAPEPLLVGLPYTVVIHYAGNLSETFHGFYKSTYRTKEGELRILASTQFEPTA
ARMAFFCFDEPAFKASFSIKIRREPRHLAISNMPLVKSVTVAEGLIEDHFDVTVKMSTYLVA
FIISDFESVSKITKSGVKVSVYAVPDKINQADYALDAAVTLEFYEDYFSIPYPLPKQDLAA
IPDFQSGAMENWGLTTYRESALLFDAEKSSASSKLGITVTVVAHELHQWFGNLTVMWENDL
WLNIEGFAKFMEFVSVSVTHPELKVGDYFFGKCFDAMEVDALNSSHPVSTPVENPAQIREMFD
DVSYDKGACILNMLREYLSADAFKSGIVQYLQKHSYKNTKNEDLWDSMASICPTDGVKMGDG
FCSRSQHSSSSSHWHQEGVDVKTMMTWTWLQRGFPLITITVGRNVHMKQEHYMKGSDGAPD
TGYLWHVPLTFITSSKNMVHRFLLTCTDVLILPEEVEWIKFNVGMNGYYIVHYEDDGWDSL
TGLLKGTHTAVSSNDRASLINNAFQLVSIKLSIEKALDLSLYLKHETEIMPVFQGLNELIP
MYKLMKMRDMNEVETQKFAFLIRLLRDLIDKQWTDEGSVSEQMLRSELLSLTACVHNYQFCV
QRAEGYFRWKESNGNLSLPVDVTLAVFAVGAQSTEGWDFLYSKYQFSLSSKEQSIEFALC
RTQNEKQLQWLLEDSEFKGDKIKTQEPFQILTLIGRNPVGYPPLAWQFLRKNWNKLQVKFELGS
SISIAHMVMGTTFNQFSTRLEEVKGFFSSSLKENGSQLRCVQQTITETIEENIGWMDKNFDKIR
VWLOSEKLERM

amino acids 1-34

amino acids 70-74, 154-158, 414-418, 760-764, 901-905

amino acids 350-360

CAGGCCACAGACGGGTCTAGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTATCCTCCCA
TGCCAGGAGTGCAGGCCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTGTCC
GACCTACCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTGCCAGGA
CACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGGTGCACGG
AGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCGGCCCTCTCCCTGATC
TCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCT
TTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCAGTCTGCTTGCTATGG
AAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCAAGGGGACCACACTGTTATGAT
GGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCC
CCAGCCAGGTGTCAACCTGCTCAATTGGGACACAGGAATTGGCCCGTGGGTATGACTGAGA
ACTGCAATAGGAAAGATTTCTGACCTGTATCGGGGAGGCCACCATTTATGAGTCAGGCAAAAC
TTGGCTCAAGAAGCCCATGATTGGACACCATCGAATACCGAGATGTGCGAGTGGGGCAGGT
GTGTGAGGAGACGCTGCTGCTCATAGATGTAGGACTCACATCAACCTGTTGGGGACAAAAG
GTGTCAGCACTGTTGGGGCTCAAAATTCCAGAAGACCACCATCCACTCAGCCCCCTCTGGG
GTGCTTGTGGCTCCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAG
CAGCGTTCTGCTGAACTCCCTCCCTCCTCAAGCTGCCCTGTCCAGGAGACCGGCAGTGTCT
CTACCTGTGTGCAGCCCCCTTGAACCTGTTCAAGTGGCTCCCCCGAATGACCTGCCCCAGG
GGCGCCACTCATTGTTATGATGGGTACATTATCTCTCAGGAGGTGGGCTGTCCACCAAAAT
GAGCATTCAGGGCTGCGTGGGCCAACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCG
GGATCTTCTCTGCGCTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGT
GGGGCTGAGGGCTGGAGTCTCTACTTGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTG
GTGGGGAGTGGTTTGCCCTTCTGCTTAACTCTATTACCCCCACGATTCTTACCAGCTGCTGA
CCACCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTC
CAATTCCTGTCATGAATCACTTCCCCACACAAATCATTATATCTACTACCTAACAGCA
ACACTGGGGAGACCTTGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTG
GCTGCATGTATCTGATAATACAGACCTGTCTTCTCA

MSAVLLLLALLGFILPLPGVQALLCQFGTVQHVKVSDLPRQWTPKNTSCDSGLGCQDTLMLI
ESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGSLISYTFVCRQEDFCNNLVNSLPLWAPQP
PADPGSLRCPVCLSMEGCLEGTTEEICPKGTTCHYDGLLRGGGIFSNLRVQGCMPQPGCN
LLNGTQEIGFVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSENTMEVGVQCQETL
LLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLNCNSASSSSVLLN
SLPPQAAPVPGDRQCPTCVQPLGTCSGSPRMTCPRGATHCYDGYIHLSGGGLSTKMSIQGC
VAQPSSFLLNHRQIGIFSAREKRDVQPPASQHEGGGAEGLESLETWGVGLALAPALWGVVC
PSC

FIGURE 251

GCGACGGGCAGGACGCCCCGTTTCGCCTAGCGCGTGCTCAGGAGTTGGTGTCTGCCTGCGCT
 CAGC**ATG**AGGGGGAATCTGGCCCTGGTGGCGTTCTAATCAGCCTGGCCCTTCTGTCACTGCTG
 CCATCTGGACATCCTCAGCCGGCTGGCGATGACGCCTGCTCTGTGCAGATCCTCGTCCCTGG
 CCTCAAAGGGGATGCGGGAGAGAAGGGAGACAAAGGCGCCCCCGGACGGCCTGGAAGAGTCG
 GCCCCACGGGAGAAAAAGGAGACATGGGGGACAAAGGACAGAAAGGCAGTGTGGGTGTCAT
 GGAAAAATTGGTCCCATTTGGCTCTAAAGGTGAGAAAGGAGATTCCGGTGACATAGGACCCCC
 TGGTCTAATGGAGAACCAGGCCTCCCATGTGAGTGCAGCCAGCTGCGCAAGGCCATCGGGG
 AGATGGACAACCAGGTCTCTCAGCTGACCAGCGAGCTCAAGTTCATCAAGAATGCTGTGCC
 GGTGTGCGCGAGACGGAGAGCAAGATCTACCTGCTGGTGAAGGAGGAGAAGCGCTACGCGGA
 CGCCAGCTGTCTGCCAGGGCCGCGGGGGCACGCTGAGCATGCCCAAGGACGAGGTGCCA
 ATGGCCTGATGGCCGCATACCTGGCGCAAGCCGGCCTGGCCCGTGTCTTCATCGGCATCAAC
 GACCTGGAGAAGGAGGGCGCCTTCGTGTACTCTGACCACTCCCCATGCGGACCTTCAACAA
 GTGGCGCAGCGGTGAGCCCAACAATGCCTACGACGAGGAGGACTGCGTGGAGATGGTGGCCT
 CGGGCGGCTGGAACGACGTGGCCTGCCACACCACCATGTACTTTCATGTGTGAGTTTGACAAG
 GAGAACAT**GTA**AGCCTCAGGCTGGGGCTGCCCATTGGGGGCCCCACATGTCCCTGCAGGGTT
 GGCAGGGACAGAGCCAGACCATGGTGCCAGCCAGGGAGCTGTCCCTCTGTGAAGGGTGGAG
 GCTCACTGAGTAGAGGGCTGTGTCTAAACTGAGAAAATGGCCTATGCTTAAGAGGAAAATG
 AAAGTGTTCCTGGGGTGTGTCTCTGAAGAAGCAGAGTTTCATTACCTGTATTGTAGCCCCA
 ATGTCATTATGTAATTATTACCCAGAATTGCTCTCCATAAAGCTTGTGCCTTTGTCCAAGC
 TATACAATAAAATCTTTAAGTAGTGCAGTAGTTAAGTCCAAAAAAAAAAAAAAAAAAAA

FIGURE 252

MRGNLALVGLISLAFLLSPSGHPQFAGDDACSVQILVPLGLKGDAKEGDKGAPGRPRGRVG
PTGEKGMGDKGQKGSVGRHGKIGPTGSKGEKDSGDTGPPGPNGEPLGPCESQLRKATGE
MDNQVSQLTSELFKIKNAVAGREKETESKIYLLVKEEKRYADAQLSCQGRGGLTSMPKDEAAN
GLMAAYLAQAGLARVFIGINLEKEGAFVYSDHSPMRTFNKWRSGEPNNAYDEEDCVEMVAS
GGMWDLVACHTTMYFCEFDKENM

AGTGACTGCAGCCTTCCTAGATCCCCCTCCACTCGGTTTCTCTCTTTGCAGGAGCACCGGCAG
CACCAGTGTGTGAGGGGAGCAGGCAGCGTCTTAGCCAGTTCCTTGATCCTGCCAGACCACC
CAGCCCCCGGCACAGAGCTGCTCCACAGGCACCA**ATG**AGGATCATGCTGCTATTACAGCCAT
CCTGGCCTTCAGCCTAGCTCAGAGCTTTGGGGCTGTCTGTAAGGAGCCACAGGAGGAGGTGG
TTCCTGGCGGGGGCCGACAGAAAGGGATCCAGATCTCTACCAGCTGCTCCAGAGACTCTTC
AAAAGCCACTCATCTCTGGAGGGATTGCTCAAAGCCCTGAGCCAGGCTAGACAGATCTCTAA
GGAATCAACATCTCCCGAGAAACGTGACATGCATGACTTCTTTGTGGGACTTATGGGCAAGA
GGAGCGTCCAGCCAGAGGGAAAGACAGGACCTTTCTTACCTTCAGTGAGGGTTCTCTGGCCC
CTTCATCCCAATCAGCTTGGATCCACAGGAAAGTCTTCCCTGGGAACAGAGGAGCAGAGACC
TTTA**TAA**GACTCTCCTACGGATGTGAATCAAGAGAACGTCCCAGCTTTGGCATCCTCAAGT
ATCCCCCGAGAGCAGAATAGGTACTCCACTTCCGGACTCCTGGACTGCATTAGGAAGACCTC
TTTCCTGTCCCAATCCCAGGTGCGCAGCTCCTGTTACCTTTCTCTTCCCTGTTCTTGT
AACATTCTTGTGCTTTGACTCCTTCTCCATCTTTTCTACGACCTGGTGTGGAACTGCA
TAGTGAATATCCCCAACCCCAATGGGCATGAGCTAGTAATACCTTAGAGTCTGTGTAGTGT
CCTACATTAAAAATATAATGTCTCTCTCTATCTCAACAATAAAGATTTTGCATATGAA
AA

FIGURE 254

MRIMLLFTAILAFSLAQSFQAVCKEPQEEVVPGGGRSKRDPDLYQLLQRLFKSHSSLEGLLK
ALSQASTDPKESTSPKSRDMHDFVGLMGKRSVQPEGKTGPFPLPSVRVPRPLHPNQLGSTGK
SSLGTEEQRPL

Important features:

Signal peptide:

amino acids 1-18

Tyrosine kinase phosphorylation site.

amino acids 36-45

N-myristoylation site.

amino acids 33-39, 59-65

Amidation site.

amino acids 90-94

Leucine zipper pattern.

amino acids 43-65

Tachykinin family signature.

amino acids 86-92

FIGURE 255

GGGCGTCTCGGCTGCTCCTATTGAGCTGTCTGCTCGCTGTGCCGCTGTGCCTGCTGTGCC
 CGCGCTGTGCGCGCTGCTACCGCGTCTGCTGGACGCGGGAGACGCCAGCGAGCTGGTGATTG
 GAGCCCTGCGGAGAGCTCAAGCGCCAGCTCTGCCCCAGGAGCCAGGCTGCCCGTGAGTC
 CCATAGTTGCTGCAGGAGTGGAGCC**ATG**AGCTGCGTCCTGGTGTTGTCATCCCCTTGGGGC
 TGCTGTTCTCGGTCTGCGGATCCCAAGGCTACCTCCTGCCCAACGTCACCTCTCTAGAGGAG
 CTGCTCAGCAAAATACCAGCACACGAGTCTCACTCCCGGGTCCGAGAGCCATCCCCAGGGA
 GGACAAGGAGGAGATCCTCATGCTGCACAACAAGCTTCGGGGCCAGGTGCAGCCTCAGGCCT
 CCAACATGGAGTACATGGTGAGCGCCGGCTCCGGCCGAGAGGCTGGCACCAGGGGTGGGGC
 CTGGGCCACAGCCTGCTCTGTTCCCGAGCAGCTCTGTTCCCCAGCCAGTGCCTGTGATGG
 CTGGCTCAGGGTCTCCTCTGGCAGGGGAGGATCCCGGCTCTGTTCTGTTTGTGTTGTTGTT
 TTGAGACAGGGTCTCACTCTGCCACTGACGCTGGAGTGCAATGGCACAAATCGTCATGCCCTG
 AAACCT**TAG**ACTCCCGGGTTAAGCGATCCTGCTTCAGCCTCCCAAGTAGCTGGAACACAG
 GCATGCACCATGGTGCCAGCTAGATTTTAAATATTTTGTGGAGATGGGGGTCTTGCTACGT
 TGCCAGGCTGGTCTTGAATCCTAGGCTCAAGCAATCCTCCTGCCTCAGCCTCTCAAAGTG
 CTAGGATTATAGGCATGAGTCAACCTGTCTGGCTCTGGCTCTGTTCTTAACATCTGCCAAA
 ACAACACACGTGGGTTCCTGTGCAGAGCCTGCCTCGTTGCCTTCATGTCACCTCTGGTAGC
 TCCACTGGGAACACAGCTCTCAGCCTTTCCACCTGGAGGCAGAGTGGGGAGGGGCCAGGG
 CTGGGCTTTGCTGATGCTGATCTCAGCTGTGCCACACGCTAGCTGCACACCCCTGACTTCTC
 CTTAGCCCGTGTGAGCCTCACTTCCACTTGGAGAGTCCTTCTCGCGTGGTTGCCATGACT
 GTGAGATAAGTCGAGGCTGTGAAGGGCCCGGCACAGACTGACCTGCCTCCCCAACCCCTAGG
 CTTTGCTAACCAGGAAAGGAGCTAACGGTGACAGAAGACAGCCAAGGTCAACCCCTCCCGGT
 GATTGTGATGGGTGTTCCAGGTGTGGTTGGGCGATGTGCTACTTGACCCCAAGCTCCAGTG
 TGAAACTTCTCTCGGCTGGTTTTCCAGAACTACAGAGGAATGGACCACAGCTCTCCAGG
 GTCCCTCCTCGTCCACCAACCGGGAGCCTCCACCTTGCCATCCGTCAGCTATGAATGGCTT
 TTTAAACAAACCCACGTCCCAGCCTGGGTAAATGGTAAAGCCCCGTCTCTACAAAAAATC
 CAAGTTAGCCGGGCATGGTGGTGCACCTGTAGTCCCAGCTGCAGTGGGACTGAGGTGGAG
 GTGGAGGTGGGGGGTGGGAGCTGAGGAAGGAGGATCGCTTGAGCCTGGGAAGTCGAGGCTGC
 AGTGAGCTGAGATTGCACCACTGCACTCCAGCCTGGGTGACAGAGCAAGACCCCTGCTCTCAAAA

FIGURE 256

MSCVLGGVIFLGLLFLVCGSQGYLLPNVTLLEELLSKYQHNEHSRVRRAIPREDKEEILML
HNKLRGQVQPQASNMEYMVSAAGSGRRGWHRGWGLGHQPALFPSQLCSPASACDGWLRVSSGR
GGSRLCSVLFVCFETGSHSATDAGVQWHNRHALKP

Important features:

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 27-31, 41-45

N-myristoylation site.

amino acids 126-132, 140-146

Amidation site.

amino acids 85-89

FIGURE 257

AAGGAGAGGCCACCGGACTTCA GTGTCTCTCCATCCAGGAGCGCAGTGGCCACT**ATG**GG
GTCTGGGCTGCCCTTGTCTCTCTTGACCCTCCTTGGCAGCTCACATGGAACAGGGCCGG
GTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCTATGAGTCCAGC
TTCTTGGAATTGCTTGAAAGCTCTGCCTCTCTCCATCTCCCTTCAGGGACCAGCGTCAC
CCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA**TGA**CAGCCATTGAAGCCTG
TGTCTTCTTGCGCCGGGCTTTTGGGCCGGGATGCAGGAGGCAGGCCCCGACCCTGTCTTT
CAGCAGGCCCCCCACCCTCCTGAGTGGCAATAAATAAAATTGGTATGCTG

FIGURE 259

AATTGTATCTGTGTAATGTTAAACAAACGAAATAAAATAGAAGAAAACTTTCTGAGTTT
CAAAAACAACAGACTAGTACTCTAAGAACTCTTTAAACAATTAAGTGTAGGATTGCAGT
TATGATTGGATATTATTTAATTCTGTTTCTGATGTGGGGTTCCTCCACTGTGTTCTGTGTGC
TATTAATATTTACCATTGCAGAAGCTTCATTCAAGTGTGAAAATGAATGCTTAGTGGATCTG
TGCCCTTTACGCATATGTTACAAATTATCTGGAGTTCCTAATCAATGCAGAGTTCCTCCCTCC
CTCCGATTGTTCTAAAT**TAA**ATTGAAAGATGTCTGCTGTGGAAAAAGGCATGTATTTAAATCTG
TATGATTCTCAACCATCTTTAGTTGGGAAAGTCCCTTGAAAGCCAATGGAAATACTTTTTTTT
TTTTCTTGGCACTAATCAAGTGAGTGTTACCTTTTCACTTAGTAGGATGTGTTGTTACGCTA
GTAAATAGAAACCTGTGTTTATTCTCAGGTATTTAGAAACAACAGCCATCATTTTATTTT
ATGTGTGTGTTCTTGGCTGTATTATAAATTATATATTTTGGGCTATCAAATATTACTTCAT
TCAATATAAATAACAATAGTAGAAGTTGTTACTTAGATATGCTTTCTAGTTGCATTTTCTC
AGCCTATGTAAGACTACTTTGTTGTAATAGCCTTTGAAATTTACAGTACTGTCTCTCTACTA
TCTTCAGATTACTTGATTCAAATAAACCAATTATGTTTGTAAATTGATATTAATAAAACCAGA
ATAAAAGTTCATATCTAGCC

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FIGURE 260

MIGYYLILFLMWGSSTVFCVLLIFTIAEASFVENECCLVDLCLLRICYKLSGVPNQCRVPLP
SDCSK

Important features:

Signal peptide:

amino acids 1-29

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FIGURE 261

GAGGATTTGGCCACAGCAGCGGATAGAGCAGGAGAGCACCACGGAGCCCTTGAGACATCCTT
 GAGAAAGAGCCACAGCATAAGAGACTGCCCTGCTTGGTGTTTTGCAGGATGATGGTGGCCCTT
 CGAGGAGCTTCTGCATTGCTGGTTCTGTTCCTTGCAGCTTTTCTGCCCCCGCCAGTGTAC
 CCAGGACCCAGCCATGGTGCATTACATCTACCAGCGCTTTCGAGTCTTGGAGCAAGGGCTGG
 AAAAAATGTACCCAAAGCAACGAGGGCATACATTCAAGAATTCCAAGAGTTCTCAAAAAATATA
 TCTGTCTAGCTGGGAAGATGTCAGACCTACACAAGTGAGTACAAAGATGCGAGTGGGTAACTT
 GGCAGTGAAGGTTGAACGTGCCAACGGGAGATTGACTACATACAACTCCTCGAGAGGCTG
 ACGAGTCATCGTATCAGAGGACAAGACACTGGCAGAAATGTTGCTCCAAGAAGCTGAAGAA
 GAGAAAAAGATCCGACTCTGCTGAATGCAAGCTGTGACAACATGCTGATGGGCATAAAGTC
 TTTGAAAAATAGTGAAGAAGATGATGGACACACATGGCTCTTGGATGAAAGATGCTGTCTATA
 ACTCTCCAAAGGTGACTTATTAAATGGATCCAGAAACAACACTGTTTGGGAATTTGCAAAAC
 ATACGGGCATTTCATGGAGGATAACACCAAGCCAGCTCCCCGGAAGCAATCCTAACACTTTT
 CTGGCAGGGAAACAGGCCAAGTGATCTACAAAGGTTTTCTATTTTTTCATAACCAAGCAACTT
 CTAATGAGATAATCAAATATAAACCCTGCAGAGAGGACTGTGGAAGATCGAATGCTGCTCCCA
 GGAGGGGTAGGCCGAGCATTGGTTTACCAGCACTCCCCCTCAACTTACATTGACCTGGCTGT
 GGATGAGCATGGGCTCTGGGCCATCCACTCTGGGCCAGGCCCATAGCCATTGGTTCTCA
 CAAAGATTGAGCCCGGCACACTGGGAGTGGAGCATTATGGGATACCCCATGCGAAGCCAG
 GATGCTGAAGCCCTCATTCTCTTGTGTGGGCTCTCTATGTGGTCTACAGTACTGGGGGCCA
 GGGCCCTCATCGCATCACTGCATCTATGATCCACTGGGCACTATCAGTGAGGAGGACTTGC
 CCAACTTGTCTTCCCCAAGAGACCAAGAAGTCACTCCATGATCCATTACAACCCAGAGAT
 AAGCAGCTCTATGCCCTGGAATGAAGGAAACCAGATCATTTACAAACTCCAGACAAAGAGAA
 GCTGCCCTCTGAAGTAAATGCATTACAGCTGTGAGAAAGAGCACTGTGGCTTTGGCAGCTGT
 TACAGGACAGTGAGGCTATAGCCCCCTTCACAATATAGTATCCCTCTAATCACACAGGAAG
 AGTGTGTAGAAGTGGAAATACGTATGCCTCTTTCCCAATGTCACTGCCTTAGGTATCTTC
 CAAGAGCTTAGATGAGAGCATATCATCAGGAAAGTTTCAACAATGTCCATTACTCCCCCAAA
 CCTCCTGGCTCTCAAGGATGACCACATTCTGATACAGCTACTTCAAGCCTTTTGTTTTACT
 GCTCCCCAGCATTTACTGTAACTCTGCCATCTTCCCTCCCAATAGAGTTGTATGCCAGC
 CCTAATATTACCAGCTGGCTTTTCTCTCCCTGGCCCTTGTGTAAGCTCTTCCCTCTTTT
 CAAATGTCTATTGATATTCTCCCATTTTCACTGCCCAACTAAAATACTATTAATATTCTTT
 CTTTCTTTTTCTTTTTTTTGGAGACAAGGTCTCACTATGTTGCCAGGCTGGTCTCAAATCC
 AGAGCTCAAGAGATCCTCTGCCTCAGCCTCCTAAGTACCTGGGATTACAGGCATGTGCCAC
 CACACCTGGCTTAAATAGTATTCTTATTGAGGTTTAACTCTATTCCCTAGCCCTGTC
 CTTCCACTAAGCTTGGTAGATGTAATAATAAAGTGAATAATTAACATTTGAATATCGCTTT
 CCAGGTGTGGAGTGTGTGCACATCATTGAATCTCGTTTCACTTTGTGAACATGCACAAG
 TCTTTACAGCTGTCACTTACAGTTTAGGTGAGTAACACAATTCAAAGTGAAGATACAGC
 TAGAAAAATCTACAAATCCCATAGTTTTCATTGCCCAAGGAGCATCAAATACGTATGTT
 TGTTCACCTACTCTTATAGTCAATGCGTTTCACTCGTTTCAAGCTTAAAAATATAGTCTGTCCC
 TTTAGCCAGTTTTCATGCTGCACAAGACCTTTCAATAGGCCCTTCAAATGATCAATTCTCTCC
 AGAAAAACAGTCTAAGGGTGAGGACCCCAACTCTAGCCTCCTCTGTCTTGTCTGCTGCTGCT
 TTCTCTCTTTCTGCTTTAAATTCAATAAAAGTGACACTGAGCAAAAAAAAAAAAAA

FIGURE 262

MMVALRGASALLVFLAAFLPPPQCTQDPAMVHYIYQRFVLEQGLEKCTQATRAYIQEFQE
FSKNISVMLGRCQTYTSEYKSAVGNLALRVERAQRIDYIQYLREADECIVSEDKTLAEMLL
QEAEEEKKIRTLLNASC DNMLGKSLKIVKKMMDTHGSMKDAVYNSPKVYLLIGSRNNTV
WEFANIRAFMEDNTKPAPRKQILTLWQGTGQVIYKGFLLFFHNQATSNEIIKYNLQKRTVED
RMLLPGGVGRALVYQHSPSTYIDLAVDEHGLWAIHSGPGTHSHLVLTKEPPTLGVEHSWDT
PCRSQDAEASFLLCGVLYVVYSTGGQGPHRITCIYDPLGTISEEDLPNLFPPKRPRSHSMIH
YNPRDKQLYAWNEGNQIIYKLQTKRKLPLK

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FIGURE 264

MELSQMSELMGLSVLLGLLALMATAAVARGWLRAGEERSGRPACQKANGFPPDKSSGSKKQK
QYQRIKKEKPPQHNFTHRLAAALKSHSGNISCMDFSSNGKYLATCADDRTIRIWSTKDFLQ
REHRSMRANVELDHATLVRFSPCRAFIVWLANGDTLRVFKMTKREDGGYTFTATPEDFPPK
HKAPVIDIGIANTGKFIMTASSDITVLIWLSKGQVLSTINTNQMNNTAAVSPCGRFVASC
FTPDVKVWEVCFGKKGEFQEVVRAFELKGHSAAVHSFAFSNDSRRMASVSKDGTWKLWDTDV
EYKKKQDPYLLKTGRFEEAAGAAPCRLALSPNAQVLALASGSSIHLYNTRRGEKEECFERVH
GECIANLSFDITGRFLASCGDRAVRLFHNTPGHRAMVEEMQGHKLRASNESTRQLQQQLTQ
AQETLKSLGALKK

Important features:**Signal peptide:**

amino acids 1-25

N-glycosylation site.

amino acids 76-80, 92-96, 231-235, 289-293, 378-382, 421-425

Beta-transducin family Trp-Asp repeat protein.

amino acids 30-47, 105-118, 107-119, 203-216, 205-217, 296-308

FIGURE 265

TGGCCTCCCCAGCTTGCCAGGCACAAGGCTGAGCGGGAGGAAGCGAGAGGCATCTAAGCAGG
CAGTGTTTTGCCTTACCCCCAAGTGACCATGAGAGGTTGCCACGCGAGTCTCAATCATGCTCC
TCCTAGTAACCTGTGCTGACTGTGCTGTGATCACAGGGGCTGTGAGCGGGATGTCCAGTGT
GGGGCAGGCACCTGCTGTGCCATCAGCCTGTGGCTTCGAGGGGTGCGGGATGTGCACCCCGCT
GGGGCGGGAGGGCGAGGAGTGCCACCCCGGCAGCCACAAGGTCCTCTTCTCAGGAACGCA
AGCACCACACCTGTCCTTGCTTGCCCAACCTGCTGTGCTCCAGGTTCCCGGACGGCAGGTAC
CGCTGCTCCATGGAAGAACATCAATTTTTAGCGCCTTGCCCTGGTCTCAGGATACCCA
CCATCCTTTTCTGAGCACAGCCTGGATTTTATTCTGCCATGAAACCCAGCTCCCATGAC
TCTCCAGTCCCTACACTGACTACCTGATCTCTTGTCTAGTACGCACATATGCACACAG
CGACAGTACCTCCCATCATGACATGGTCCCCAGGCTGGCCTGAGGATGTACAGCTTGTAGG
CTGTGGTGTGAAGAGTGCCAGCCTGGTTCTCTCCCTGCTCAGGCTGCCAGAGAGGTGGTA
AATGCGAGAAAGGACATTCCTCCCTCCCTCCCGAGGTGACCTGCTCTCTTCTGGGCCGTG
CCCCCTCTCCACATGTATCCCTCGGTCTGAATTAGACATTCCTGGGCACAGGCTCTTGGGT
GCATTGCTCAGAGTCCCAGGTCCTGGCCTGACCCTCAGGCCCTTACGTTAGGTTCTGTGAGG
ACCAATTTGTGGGTAGTTCATCTTCCCTCGATTGGTTAACTCCTTAGTTTACAGACCAGAG
TCAAGATTGGCTCTTCCAGAGGGGCAGCAGACGTACCCCCAAGGCAGGTGTAGGGAGCCCA
GGGAGGCCAATCAGCCCCCTGAAGACTCTGGTCCAGTACGCTGTGGCTTGTGGCCTGTGA
CCTGTGACCTTCTGCCAGAATTGTATGCTCTGAGGCCCTCTTACCACACTTTACCAGT
TAACCACTGAAGCCCCCAATTCACAGCTTTTCCATTAAAAATGCAATGGTGGTGGTTCAA
TCTAATCTGATATTGACATATTAGAAGGCAATTAGGGTGTTCCTTAAACAACCTCTTCCA
AGGATCAGCCCTGAGAGCAGGTGTGGTGACTTTGAGGAGGGCAGTCTCTGTCAGATTGGGG
TGGGAGCAAGGACAGGGACAGGGCAGGGGCTGAAGGGGCACTCCCTGACACAGGAGG
CAACTACACCAACATCTGTGGCTTTAGATAAAGACCAACTGAAAAA

FIGURE 266

MRGATRVSIIMLLLVTSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEETCH
GSHKVPFFRKRKHHTCPCLPNLLCSRFPDGRYRCMDLKNINF

Signal peptide:

amino acids 1-19

Tyrosine kinase phosphorylation site:

amino acids 88-95

N-myristoylation sites:

amino acids 33-39, 35-41, 46-52

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FIGURE 267

AGCGCCCGGGCGTCGGGGCGGTAAAGGCGCGGCAGAGGAGGCACTTGAGAAATGTCTTTC
 CTCACAGGACCCAGTTTCTTACCATTGGGGATGTGGTCCATTGGTGCAGGAGCCCTGGGGC
 TGCTGCCTTGGCATTGCTGCTTGCCAACACAGACGTGTTTCTGTCCAAGCCCAGAAAGCG
 CCCTGGAGTACCTGGAGGATATAGACCTGAAACACTGGAGAAGGAACCAAGGACTTTCAAA
 GCAAAGGAGCTATGGGAAAAAAATGGAGCTGTGATTATGGCCGTGCGGAGGCCAGGCTGTT
 CCTCTGTCGAGAGGAAGCTGCGGATCTGTCTCCCTGAAAAGCATGTTGGACCAGCTGGGCG
 TCCCCCTCTATGCAGTGGTAAAGGAGCACATCAGGACTGAAGTGAAGGATTTCCAGCCTTAT
 TTCAAAGGAGAAATCTTCTGGATGAAAAGAAAAAGTTCTATGGTCCACAAGGCGGAAGAT
 GATGTTTATGGGATTTATCCGTCTGGGAGTGTGGTACAACTTCTTCCGAGCCTGGAACGGAG
 GCTTCTCTGGAACCTGGAAGGAGAAGGCTTCATCCTTGGGGGAGTTTTCGTGTTGGGATCA
 GGAAAGCAGGGCATTCTTCTTGAGCACCGAGAAAAAGAAATTGGAGACAAAGTAAACCTACT
 TTCTGTTCTGGAAGCTGCTAAGATGATCAAACCACAGACTTTGGCCTCAGAGAAAAATGAT
 TGTGTGAAACTGCCAGCTCAGGGATAACCAGGGACATTCACCTGTGTTTCATGGGATGTATT
 GTTTCCACTCGTGTCCCATAAGGAGTGAGAAACCCATTATATACTCTACTCTCAGTATGGATTA
 TTAATGTATTTTAATATTCTGTTTAGGCCCACTAAGGCAAAATAGCCCCAAAAACAAGACTGA
 CAAAAATCTGAAAAACTAATGAGGATTATTAAGCTAAACCTGGGAAATGAGAGGCTTAAAA
 TTGACTGCCAGGCTGGGTGCAGTGGCTCACACCTGCAATCCAGCACTTTGGGAGGCCAAGG
 TGAGCAAGTCACTTGAGTCCGGGATCTCGAGACAGCCTGAGCAACATGGCGAAACCCGTC
 TCTACTAAAAATACAAAAATCACCCTGGGTGTGGTGGCAGGCACCTGTAGTCCCAGCTACCCG
 GAGGCTGAGGCAGGAGAAATCACTTGAACCTGGGAGGTGGAGGTGCGGTGAGCTGAGATCA
 CACCACTGTATTCAGCCTGGGTGACTGAGACTCTAACTAA

FIGURE 268

MSFLQDPSFFTGMWSIGAGALGAAALALLANTDVFLSKPQKALEYLEDIDLKTLKEEPR
TFKAKELWEKNGAVIMAVRRPGCFLCREEAADLSSLKSLDQLGVPLYAVVKEHIRTEVKDF
QPYFKGEI FLDEKKKFYGPQRRKMMFMGFIRLGWVYNFFRAWNGGFSGNLEGE GFILGGVFV
VGSGKQGILLEHREKEFGDKVNLLSVLEAAKMIKPQTLASEKK

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ACGGACCAGAGGGTTCGAGGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCCG
GGCCAGGTGCCCGTCGACAGGTGCCCTTGGCCGGAGATGCGGTAGGAGGGGCGAGCGCGAGA
AGCCCCCTTCTCGGCGCTGCCAACCCGCCACCCAGCCATGGCGAACCCGGGCTGGGGCTG
CTTCTGGCGCTGGGCCTGCCGTTCTGCTGGCCGCTGGGGCCGAGCCTGGGGGCAATACA
GACCACTTCTGCAAAATGAAATAGCACTGTTTTGCCTTCATCCACCAGCTCCAGCTCCGATG
GCAACCTGCGTCCGGAAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTTGGCTGCCCTG
CTCCTGGCTGTGGGGCTGGCACTGTTGGTGCGGAAGCTTCGGGAGAAGCGGCAGACGGAGGG
CACCTACCGGCCAGTAGCGAGGAGCAGTTCTCCCATGCAGCCGAGGCCCGGGCCCCCTCAGG
ACTCCAAGGAGACGGTGCAGGGCTGCCCTGCCCATTAGTCCCTCTCTCTGCATCTGTTCTTC
CTTCAATGTCTGTGTACCTTGGGGAAGGACGCTGCCCTCTCTGGGCAGTCAGATCCACCCAG
TGCTTAAATAGCAGGGAAGAAGGTACTTCAAAGACTGCCCGCCCTGAGGTCAAGAGAGGATGGG
GCTATTACATCTTTATATATTTATATAAAATTAGTAGTGAGATGTAAAAAAAAAAAAAAAAAA

270/330

FIGURE 270

MANPGLGLLLALGLPFLLARWGRAWGQIQTTSANENSTVLPSTSSSSDGNLRPEAITAIIV
VFSLLAALLLAVGLALLVRKLRKRQTEGTYRPSSEEQFSHAAEARAPQDSKETVQGCLPI

09990440.111401

FIGURE 271

AATATATCATCTATTATTATCATTAATCAATAATGTATTCTTTTATTCCAATAACATTGGGTT
TTGGGATTTTAATTTTCAAACACAGCAGAAATGACATTTTTCTGTCACTATTATTATTGTTG
GTATGTGAAGCTATTTTGGAGATCCAATTCAGGAAGCAACACATTGGAGAATGGCTACTTTCT
ATCAAGAAATAAGAGAAACCACAGTCAACCCACACAATCATCTTTAGAAGACAGTGTGACTC
CTACCAAAGCTGTCAAACCACAGGCAAGGGCATAGTTAAAGGACGGAATCTTGACTCAAGA
GGGTAAATCTTGGTGTGAAGCCTGGGGCAGGGGTGTAAGAAAAACACTTAGATTCAATG
ATTGTAAATTTAAGGCAAATACACATATTAGTATTACCTTAGTGTAATGTATCCCTGTCATA
TATACAATAAGGTGAAATTTAAGTACCCTATGCAGTTGGCTGGACAGTTCTAAATTGGACT
TTATTAATTTTTAAATCAGTAACTGATTATCACTGGCTATGTGCTTAGATCTACAGGAGA
TCATATAATTTGATACAAATAAAAGAAAGTGTCTCTCCCTTACGAATTGACATTTTAA
ATCGATACAGTTAGAATAGGAATATGACATTAGAAAGGAAGAATGACAGGAGAAAGGAA
AGAAGGGAAAATGTTGCCAAGGAAAAAATAA

FIGURE 273

GCCAGGAATAACTAGAGAGGAACA**ATG**GGGTTATTAGAGGTTTGTGTTTCCTCTTAGTTCT
 GTGCTCTGTCACCACTCAATACTTCTCTTCAATTAAGCTGAATAATAATGGCTTTGAAGATA
 TTGTCAATTGTTATAGATCCTTAGTGTGCCAGAAGATGAAAAATAATTTGAACAAATAGAGGAT
 ATGGTGACCTACAGCTTCTACGTACCTGTTTGAAGCCACAGAAAAAGATTTTTTTTCAAAAA
 TGTATCTATATTATCTCCGAGAATTGGAAGGAAAAATCCTCAGTACAAAAGGCCAAACATG
 AAAACCATAAACATGCTGATGTTATTAGTTGCACCACCTACACTCCCAGGTAGAGATGAACCA
 TACACCACAGCAGTTACAGAAATGTGGAGAGAAGGCCAATACATTCACTTCACTCCCTGACCT
 TCTACTTGGAAAAAACAATAATGAATATGGACCACAGGCAAACTGTTTGTCCATGAGTGGG
 CTCACCTCCGGTGGGGAGTGTTTGATGAGTACAATGAAGATCAGCCTTTCTACCGTCTAAG
 TCAAAAAATAATCGAAGCAACAGGTGTTCCGCAAGTATCTCTGGTAGAAATAGAGTTTATAAG
 GTGTCAAGGAGGCGAGCTGTCTTAGTAGAGCATGCAGAATTGATTCTACAACAAAACGTGTATG
 GAAAAGATTGTCAATTCCTTCTGATAAAGTACAAAACAGAAAAAGCATCCATAATGTTTATG
 CAAAGATTGATTCTGTGTTGCAATTTTGTAAACAAAAACCCATAATCAAGAAGCTCCAAG
 CCTACAAAACATAAAGTGCAATTTAGAAGTACATGGGAGGTGATTAGCAATTTCTGAGGATT
 TTAATAAACACCATACCCATGGTGACACACCTCTCCACCTGTCTTCTCATTGCTGAAGATC
 AGTCAAAAGAAATTGTGCTTAGTCTTGATAAGTCTGGAAGCATGGGGGGTGAAGACCGCT
 AAATCGAATGAATCAAGCAGCAAAAACATTTCTGCTGCAGACTGTTGAAAATGGATCCTGGG
 TGGGATGTTCACTTTGATAGTACTGCCACTATTGTAATAAGCTAATCCAAATAAAAAAGC
 AGTGATGAAGAAGAACACACTCATGGCAGGATTACCTACATACCTCTGGGAGAACTTCCAT
 CTGCTCTGAATTTAAATATGCATTTCAAGTGATTGGAGAGCTACATTCCCAACCTCGATGGAT
 CCGAAGTACTGCTGCTGATGATGGGAGGATAACACTGCAAGTTCTTGATTTGATGAAGTG
 AAACAAAGTGGGGCATTGTTCTATTTATGCTTTGGGAAGAGTGCTGATGAAGCAGTAAAT
 AGAGATGAGCAAGATACAGGAGGAAGCTTTTATGTTTCAGATGAAGCTCAGAACATG
 GCCTCATTTGATGCTTTTGGGCTCTTACATCAGGAATACTGATCTCTCCAGAACTCCCTT
 CAGCTCGAAAGTAAGGGATTAAACACTGAATAGTAATGCCTGGATGAACGACACTGTCATAT
 TAGATGACAGTGGGAAGGACACGTTCTTTCTCATCACATGGAACAGCTGTGCTCTCCAGTA
 TTTCTCTCTGGGATCCAGTGAACAAATAATGAAAAATTCACAGTGGATGCAACTTCCAAA
 TTGGCCTATCTAGTAATCCAGGAATGCNAAGTGGGCACTGGGCATACAATCTTCAAGC
 CHAAGCGAACCAGAAACATTAACATTACAGTAACCTCTCGAGCAGCAAAATCTTCTGTGCT
 CTCCAATCAGATGAATGCTATAAATGAATAAGGACGTAACAGTTTCCCCAGCCCAATGATT
 GTTTACGCAGAAATCTACAAGGATATGTACCTGTTCTTGGAGCCAATGTGACTGCTTTTAT
 TGAATCACAGAAATGGACATACAGAAGTTTGGAACTTTTGGATAATGGTGCAGGCGCTGATT
 CTTTCAAGATATGAGGACTCTACTCCAGGTATTTACAGCATATACAGAAAAATGGCAGATAT
 AGCTTAAAGTTCTGGGCTCATGGAGGAGCAAACTGCCAGCTAAAATTACGGCTCCCAT
 GAATAGAGCGCGCTACATACCGCTGGGTAGTGAACGGGGAATTAAGCAAAACCCGCAAA
 GACCTCGAAATGATGAGGATACTCAGACCCTTGGAGGATTTCAGCGCAACAGCATCCCGGA
 GGTGCAATTTGTGGTATCACAAGTCCCAAGCCTTCCCTTGCTGACCAATACCCCAAGTGA
 AATCACAGACCTTGATGCCACAGTTTCAAGGATAAGATTATCTTACATGGACAGCACCAG
 GAGATAAATTTTGTGTTGCAAAAGTTCAACGTTATATCATAGAATAAGTGCAAGTATCTT
 GATCTAAGACAGCTTTGATGATGCTCTTCAAGTAAATACTACTGATCTGTCAACAAAGGA
 GCGCAACTCCAGGAAGAGCTTTCGATTTAAACCAAGAAATCTCAGAGAAATGCAACCC
 ACATATTTATTGCCATTAAGATATAGATAAAAGCAATTTGACATCAAAAGTATCCAACTT
 CCTCAAGTAACCTTTGTTTCTCCCTCAAGCAATCTGATGACATTGATCTACACTGCTATCC
 TGTCTCTACTCTCTCTGTAATAAGTCAATTTCTGGAGTTAATATTTCTACGCTGGTAT
 TGCTGTGATTGGGTCTGTTGTAATTTGTAACCTTTATTTAAGTACCACTT**TGA**ACCTTA
 ACGAAGAAAAAATCTTCAAGTAGACCTAGAAGAGAGTTTAAAAAACAAAAAATGTAAGT
 AAAGGATATTCTGTAATCTTAAATATCATCCCATGTGTGATCATAACTCATAAAAAATAAT
 TTAAGATCTCGAAAGAGGATACTTTGATTAATAAAAAACACTCGGATATGTAATAACTGT
 CAAGATTAATAATTAATGTTTCAATTTATTTGTTATTTTATTTGTAAGAAATGATGTAAC
 AAGATCTCTTTTCACTACTGATACCTGGTTGTATATTTTATGATGCAACAGTTTCTGAAAT
 GATATTTCAAAATGGATCAAGAAATTAATAATCATCTATCTAGTAGTCAAAATACAAGTAAA
 GGAGAGCAAAATAAACACATTTGGAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
 AA

MGLFRGFFVLLVLCLLHQNSTSFIKLNNGGFEDIVIVIDPSVPEDEKIEIQIEDMVTTASTY
LFEATEKRFFFKNVSILIENWKENPOYKRPKHENHKKHADVIVAPPTLPGRDEPYTKQFTEC
GEKGEYIHTPDLLLGKKQNEYGPPGKLFVHEWAHLRWGVFDEYNEDQPFYRAKSKKIEATR
CSAGISGRNRVYKQGGSCLSRACRIDSTTKLYGKDCQFFPDVKVQTEKASIMFMQSIDSVVE
FCNEKTHNQEAPSLQNIKCNFRSTWEVISNSEDFKNTIPMVTPPPPVFSLLKISQRIVCLV
LDKSGSMGGKDRLNRMNQAAKHFLQLTVENGSWFGMVHFDSTATIVNKLIQIKSSDERNTLM
AGLPTYPLGGTSICSGIKYAFQVIGELHSQLDGSSEVLLTLDGEDNTASSCIDEVKQSGAIVH
FIALGRAADEAVIEMSKITGGSHFYVSDEAQNNGLIDAFGALTSNGTDLSQLQLESKGLT
LNSNAWMNDTVIIDSTVGKDTFFLITWNSLPPSISLWDPSTGTIMENFTVDATSKMAYLSIPG
TAKVGTWAYNLQAKANPETLTTITVTSRAANSSVPPITVNAMKNKDVSFSPSMIVYAEILQG
YVPVLGANVTAFIGESQNGHTEVLELLDNAGADSFKNDDGVYSRYFTTENTENGRYSCLKVRAHG
GANTARLKLRPPLNRAAYIPGWVWNGEIANPPREIDEDTQTYATEDFSRTASGGAFVVSQV
PSLPLPDQPPSQITDLDATVHDEKIILTWPAGNDFDVGKQRYIRISASILDLRDSFDD
ALQVNTTDLSPKEANSKESFAKPENISEENATHIFIAIKSIDKSNLTSKVSNIAQVTLTFIP
QANPDDIDTPTPTPTPTPKSHNSGVNISTLVLSVIGSVVIVNFILSTTI

amino acids 1-21

amino acids 284-300, 617-633

amino acids 469-491, 476-498

amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592,
628-632, 811-815, 832-836, 837-841, 852-856, 896-900

FIGURE 275

CTCCTTAGGTGGAACCTGGGAGTAGAGTACTGACAGCAAAGACCGGGAAAGACCATACGTCCTCCG
 GGCAGGCTGACAAACAGGTGTTCATCTTTTGGATCTCGTGTGTGGCTGCCTTCTTATTTCAAGGAAAG
 AGCCCAAGGTAAATTTGATCCACAGAGGAGCAATGATGAGCCACCTCCTAACCTTCCCTCTTTGAACC
 CCCAGTTATGCGCAGGATTTACTAGAGAGTGTCAACTCAACCAGCAAGCGGCTCCTTCGGCTTTAACTTT
 GTGGTTGAGAGAGAACCTTTGTGGGGCTGCGTTCTCTTACGATGCTCAGAGTGACTCAGAGTCTTGCTGA
 GGGTGGACGAGAAAGAAAGGAAGGTCCCCCTTCTGCTGTGGCTGCGACTCAGGAAGGCTGTGATGGG
 AATGAAGGCTGAAACTCTGGAGATTTCACTTCAGTCATTTGCTTCTGCTGCAAGATCATCTCTTTAAAA
 GTAGAGAAGCTGCTCTGTGTGGTGGTTAACTCCAAGAGGCGAGAAGCTCGTTCTAGAAGGAAATGGATG
 CAAGCAGCTCCGGGGGGCCAAACCGCATGCTTCTGTGGTCTAGCCACGGGAAGCCCTTCGTGGGG
 GCCCCGGCTTTGAGGGATGCCACCGGTTCTGGAGCGATGGCTGATTCCTGAATGAATGATGGTTCCGC
 GGGGGCTGCTTGGCTGGATTTCCCGGGTGGTGGTTTGTGTTGGTCCCTCTCTGTGCTCTCTCTGT
 CCTGTACATCTTGGGCTGCACCCCAAAGGTGACGAGGACACTGGCACTGCTCCAGGGCCAAACAGC
 CCCAGCGGGAAGGAGGGGTACCCAGGCCCTCTTCCAGGATGGGAGGACGACCCCACTACGTGA
 CGAGCCTGAACGGGAGATCCAGCAGCTCAAGGAGGAGCTGCAGGAGGAGGTGAGCAGCTCAGGAA
 TGCGCAGTACCAAGCCAGCATGCTGCTGGCCTGGGCTGCGAGGAGCCCCCAGAGAAACCCAG
 GCCACCTCTTGGCTTCTGCTCACTCGCAGGTGGACAAGGCAGAGTGAATGCTGGCTCAAGCTGG
 CCACAGAGTATGCAGCAGTGCTTTTCGATAGCTTTACTCTACAGAGGTTTACCAGCTGGAGACTGG
 CCTTACCCCGACCCCGAGGAGAAGCCTGTGAGGAGGACAAGCGGGATGATTTGGTGGGAAGCCATT
 GAATCAGCCTTGGAGACCTTGAACAATCCTGCAGAGAACAGCCCCAATCACCCTGCTTACACGGCTC
 CTGATTTTCATGAAGGGATCTACCGGAACAGAAAGGACAAGGGACATTTGATGAGCTCACTTTCAA
 AGGGGACCAACAAACGCAATTTCAACAGGCTCATCTTATTCGACCACTCAGCCCCATCTGAAGAGT
 AAAAAAGAAAGCTCAACATGGCCCAACACGCTTATCAATGTATCTGCTGCTCTAGCAAAATCTGG
 ACAAGTTCGGCAGCTTATCGAGAAATTCAGGGAGATGTGCATTTGACGACGATGGGATGGATGGT
 CCACTGTGTTTACTTTGGGAAGAAAGAAATTAATCAAGTCAAGGAATCTGAAGAACACTTCCAAA
 GCTGCGCACTTCAGGAATCTTACCTTTCATCAGCTGATGAGAATTTCTCGGGGAAGAGGACTTG
 ATGTTGGAGCCCGCTTCTGGAGGGAAGCAACGCTCCTTCTCTTTCTGTGATGTGACATCTTACTT
 CACATCTGAATTTCTCAATACGCTGTAGGCTGAATCACACAGCAGGGGAAGAGGTATTTATTCAGATT
 CTTTTCAGTCAAGTAACTCTGGCATTAATATACGGCCACCATGATGCAAGTCCCTCCTTGGAAACAGC
 AGCTTGTGTCATAAAGAGGAAACCTGGATTTTGGAGAGACTTTGATTTGGGATGACGTGTCAAGTATCG
 GTCACTTTTCATCAATATAGGTGGGTTTGTCTGGACATCAAGAGCTGGGGCGGAGAGGATGTGCAC
 CTTTATTCGAAGTATCTCCACAGCAACCTCATAGTGGTACGGACGCTGTGCGAGGACTCTCCACC
 TCTGCGATGAGAAGCGCTGCATGGACGAGCTGACCCCCGAGCAGTACAAGATGTGCATGAGCTCCAA
 GGCCATGAACAGGAGCTCCACCGCCAGCTGGGCATGCTGGTGTTCAGGCACGATGAGGAGGCTCAC
 CTTTCGCAACAGAAACAGAGCAAGTAGCAAAAAACATGACTCCCGAGAGAGGATGTGGGGA
 CACTTTTCTTCTTCTTCTGCAATTACTGAAAGTGGCTGCACAGAGAAAGACTTCCATAAGAGAGC
 ACAGAAAGATTTGGACTGTGGGTGAGAGATGAGAAGGCTCCGATTTCTCTGCTTGGGCTTTTAC
 AACAGAAATCAAAATCTCCGCTTTGCTGCAAAAGTAACCCAGTGGCAGTGTGAGATGTCTGACA
 AAGGCAGAAATGCTTGTGAGATTAAGCCTTAAGCTTAAATATTCATGATTTAAGAGCAGTTTGTAAAAATTCAT
 TAGCATGAAGAGCAACGATATTTCTCCTTGAATATTCATGATTAAGAGGCTCAGCAGGGCTCTAGTTTCTAGG
 AATGCTAAAAATTCAGAAAGGAGGAGAGGATAGGCTTATTATGATAGTGAAGTACATTAAGTA
 AATAAATAATGGACAGAGGAAAGAAACCAATCAATATCGTGTATATTTCCCAAGATTAAACCA
 AAAATAATCTGCTTATCTTTTGGTGTCTTTTAACTGTCTCCGTTTCTTTTCTTTTAAAAAT
 GCACTTTTTTCTTGTGTGAGTTATAGTCTGCTTATTTAATTACCACTTTGCAAGCCTTACAAGAGA
 GCACAAGTTGGCTCATTTTATTTTAAAGAGATCTTTGAGATGATTTATGAGAACTTTCAT
 GTTCAAGGATCAAAATGATGCCATATCCAGGACATGCCAAATGCTGTCTGTCTGACGACCTTCTCGAA
 GTCAGGCATTGAGACATAGGGAAGGAATGGTTTGTACTAATACAGCGTACAGTACATCTCTCTGAA
 GAGTATTTTTCGAAGGAGGACCACTGAACCTGGAGGAAGAGAAATGACACATTTTCTCTCA
 AAGGAAACTCATTCAGACTGGTGATATCTGATGATACCTAAGTTCAGGACCTTCTGTCAGGCACGAT
 GAGTATGAGGACCTTCTCTCTCTTTAAATAAACCAAGATTAACGCTGTGAACCAACAACTCTCT
 TTTCAAAACAGGCTTCTCTCTCTGCTTCTGCTTCAACAGGAGAAATGAGAAATATATATAT
 ATATATATATATTTGGAAGAGCTCAATCCATCTGCCAGAACTAGTGGGATGGAAGTTTGTGCTACAT
 GTTATCCACCCAGGAGAGGTGGAAGTAACCTGAATTTTAAATTAAGCAGTCTTACTCAATCA
 CCAAGATGCTTGTGAAATTTGATTTTATTACCATTTCAAACATTTTAAAAATTAATACAGTTA
 ACATAGAGTGGTTCCTTCTTCACTGTGAAATTTATAGCCAGCAGCATGAGTCACTGAATATCT
 CTTTGTGCTTGTCTGTTTGTCTGCTCAAGTAACTCATTGTTTAAAGCTTCAAGAACATTTCAAGC
 TGTGTGGTGTGTTAAAAAATGCATTTGTATTTGATCTGATTTGATTTGAATTTTAAATAAAAAC
 AGGCCATGAATGGAAGGTGGTATTCACAGCTAATAAAATATGATTTGTGATATGA

FIGURE 276

MMVVRGLLAWISRVVLLVLLCCAISVLYMLACTPKGDEEQALALPRANSPGKEGYQAVLQ
EWEEQHRYNVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADLLAFL
HSQVDKAEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPEEKPVKDKRDELVEAIES
ALETNNPAENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLILFRPFSP
MKVKNKELNMANTLINVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKEEINEVK
GILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTR
LNTQPGKKVFYPVLFSQYNPGIYGHHDVPPLEQQLVIKKETGFWRDFGFGMTCQYRSDFI
NIGGFDLDIKGWGGEDVHLYRKYLSNLIVVRTPVRLFHLWHEKRCMDELTPQYKMCMQS
KAMNEASHGQLGMLVFRHEIEAHLRKQKQKTSSKKT

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GGAAGAATGTTGTGGCTGCTCTTTTTCTGGTGACTGCCATTGCTGAACCTGTGCAAC
AGGTGCAGAAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCAT
ATGCGCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA
GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCTACTTTGCAATGTAACCCAGAGGGT
ATCATTCTGGTTTGTGGTTACAGACCCCTTCAAAAAATCACACCTTCTCTGCTGTTGAGGTGC
AATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAAACCT
CTGGAATTTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTGCCCATCTG
GATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACACTACTGATTTTAT
CAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGATGACGCTGAAGAT
AAGTGTGAAACATGATCACAAATGAAAAATGGCATCCCCCTCTGATCCCCCTGGACATGAAGGG
GGGCATATTAATGATGCCTTCACTGACAGAGGATGAGAGGCTCACCCCTCTCTGAAGGGCTGT
TGTTCTGCTTCTCAAGAAATTAACATTGTTTCTGTGTGACTGCTGAGCATCTGAAATA
CCAAGAGCAGATCATATATTTTGTTCACCATCTCTTCTTTGTAATAAAATTTGAATGTGCT
TGAAAGTGAAAGCAATCAATTATACCCACCAACACCACTGAAATCATAAGCTATTCACGAC
TCAAAATATTTCTAAAATATTTTTCTGACAGTATAGTGTATAAATGTGGTCATGTGGTATTG
TAGTTATTGATTTAAGCATTTTTAGAAATAAGATCAGGCATATGTATATATTTTCACACTTC
AAAGACCTAAGGAAAAATAAATTTTCCAGTGGAGATACATATAATATGGTGTAGAAATCAT
TGAAATGGATCCTTTTGCAGCATCACTTATACCTCTGTATATGCAATAGTAAGTAACAAAG
TGAGAAGTAATTATTGTAAATGGATGGATAAAATGGAATTACTCATATACAGGGTGGAAAT
TTATCTGTATTACACCAACAGCTTGATTATATATTTTCTGAATATCAGCCCCATAAGGAC
AATTCATTATTGTGACCAATTTCTACAATTTGTAAAAAGTCCAATCTGTGCTAACTTAATAAAG
TAATAATCATCTCTTTTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

AACCTCAAACCTCCTCTCTCTCTGGGAAACACGGGTGCTTGCTCCTCCCGAGTGGCCTTGGCAGG
GTGTTGGAGCCCTCGGTCTGCCCGTCCGGTCTCTGGGGCCAAGGCTGGGTTTCCCTC**ATGT**
ATGGCAAGAGCTCTACTCGTGCGGTGCTTCTTCTCCTTGGCATACAGCTCACAGCTCTTTGG
CCTATAGCAGCTGTGGAAATTATACCTCCCGGGTGCTGGAGGCTGTTAATGGGACAGATGC
TCGGTTAAAAATGCACTTTCTCCAGCTTTGCCCTGTGGGTGATGCTCTAACAGTGACCTTGG
ATTTTCGTCTCTAGACGGGGGACCTGAGCAGTTTGTATTCTACTACCACATAGATCCCTTC
CAACCCATGAGTGGGCGGTTTAAGGACCGGGTGCTTGGGATGGGAATCCTGAGCGGTACGA
TGCTCCATCCTTCTCTGGAAATGCAGTTCGACGACAATGGGACATACCTGCCAGGTGA
AGAACCACCTGATGTTGATGGGTGATAGGGGAGATCCGGTCTACGCGTCGTGCACACTGTA
CGCTTCTCTGAGATCCACTTCTTGCTCTGGCCATTGGCTCTGCCTGTGCACTGATGATCAT
AATAGTAATTGTAGTGGTCTCTTCAGCATTACCGGAAAAAGCGATGGGCCGAAAGAGCTC
ATAAAGTGTGGAGATAAAATCAAAAGAAGAGGAAAGGCTCAACCAAGAGAAAAAGGTCTCT
GTTTATTTTAGAAGACACAGAC**TAA**CAATTTTAGATGGAAGCTGAGATGATTTCGAAGACAA
GAACCCTAGTATTTCTTGAAGTTAATGGAACCTTTTCTTTGGCTTTTCCAGTTGTGACCCGT
TTTCCAACAGTTCTGCAGCATATTAGATTCTAGACAAGCAACACCCCTCTGGAGCCAGCAC
AGTGCTCCTCCATATACCCAGTCATACACAGCCTCATTATTAAGGTCCTATTATTAATTTGAG
GTGTAATATTTTTCAAGTGCTCATTAGGTTTTATAAACAAGAAGCTACATTTTTGCCCTTAA
GACACTACTTACAGTGTTATGACTTGATACACATATATTGGTATCAAAGGGGATAAAGCC
AATTTGTCTGTTACATTTCCCTTTCACGTATTTCTTTTAGCAGCACTCTCGCTACTAAAGTTA
ATGTGTTTACTCTCTTCCCTCCCACATTTCTCAATTAAGGTTGAGCTAAGCCTCCTCGGTG
TTTCTGATTAAACAGTAAATCCTAAATTCAAAGCTGTTAAATGACATTTTTATTTTTATGTCTC
TCCTTAACATATGAGACACATCTTGTTTTACTGAATTTCTTTCAATATTCAGGTGATAGATT
TTTGTGCG

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FIGURE 280

MYGKSSTRAVLLLLLGIQLTALWPAAVEIYTSRVLEAVNGTDARLKCTFSSFAPVGDALTVT
WNFRPLDGGPEQVFVYYHIDPFQPMSEGRFKDRVSWDGNPERYDASILLWKLQFDDNGTYTCQ
VKNPPDVGVIGEIRLSVVHTVRFSEIHFLALALGSAALMIIIVIVVVLQHYRKKRWAER
AHKVVEIKSKEERLNQEKVSVYLETD

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FIGURE 281

GCATTTTTGTCTGTGCTCCCTGATCTTCAGGTACCACCATGAAGTCTCTAGCAGTCTGGT
ACTCTTGGGAGTTTCCATCTTTCTGGTCTCTGCCAGAATCCGACAACAGCTGCTCCAGCTG
ACACGTATCCAGTACTGGTCTGTGATGATGAAGCCCTGATGCTGAAACCACTGCTGCT
GCAACCACCTGCGACCACTGCTGCTCTACCACTGCAACCACCGTGCTTCTACCACTGCTCG
TAAAGACATTCCAGTTTTACCCAAATGGGTGGGGATCTCCCGAATGGTAGAGTGTGCTCCCT
GAGATGGAATCAGCTTGAAGTCTTCTGCAATTGGTCACAACATTTATGCTTCTGTGATTTC
ATCCAACTACTTACCTTGCCACGATATCCCTTTATCTCTAATCAGTTTATTTCTTTCAA
ATAAAAAATAACTATGAGCAACATAAAAAAAAAAAAAA

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FIGURE 282

MKFLAVLVLLGVSI FLVSAQNPTTAAPADTYPATGPADDEAPDAETTAAATTATTAAPTAT
TAASTTARKDIPVLPKWVGDLNGRVCP

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FIGURE 283

GGACTCTGAAGGTCCCAAGCAGCTGCTGAGGCCCCCAAGGAAGTGGTTCCAACCTTGGACCC
CTAGGGGTCTGGATTTGCTGGTTAACAAGATAACCTGAGGGCAGGACCCCATAGGGGA**ATGC**
TACCTCCTGCCCTTCCACCTGCCCTGGTGTTACGGTGGCCTGGTCCCTCCTTGCCGAGAGA
GTGTCCCTGGGTCAGGGACGCAGAGGACGCTCACAGACTCCAGCCCTTTGTTACCGAGAGGAC
ACTTGGCAAGGTCCAGCGATGGTCCGGAGTCCACACACAGACTGGCGGCAGGGCAGGAGGGG
GACAGTTCTGTTGTGCTTGGTTGGACAGTAAGAGGGTCTTGGCCAGTCCAGGGTGGGGGGCG
GCAAACTCCATAAAGAACCAGAGGGTCTGGGCCCCGGCCACAGAGTCATCTGCCCAGCTCCT
CTGCTGCTGGCCAGTGGGAGTGGCACGAGGTGGGGCTTTGTGCCAG**TAAA**AACCACAGGCTGG
ATTTGCCTGCGGGCCATGGTCCCTGTCTAGGGCAGCAATTCTCAACCTTCTTGCTCTCAGGA
CCCCAAAGAGCTTTCATTGTATCTATTGATTTTTACCACATTAGCAATTAAAACTGAGAAAT
GGGCCGGGCACGGTGGCTCACGCCTGTAATCCAGCACTTTGGGAGGCCGAGGCGGGTGGAT
CACCTGAGATCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAACCTTGTCTACTAAAAA
TACAAAAAATTAGCCAGGCACAGTGGTGTGCACCTGGTAGTCCAGTTACTCGGGAGGCTGAG
GCAGGAAAAATCGCTTGAACCCAGGAGCGGACGTTGCGGTGAGCCGAGATCGCGCCGCTGAT
TCCAGCCTGGGCGACAAGAGTGAGACTCCATCTCACACA

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GTCTATGCGCCAGTGCCTGCTCTGTGCTGCTCTGGGCCCTGGCAATGGTGACCGGCCTGCCTCA
GCGGCCCCCATGGGCGGCCAGAACTGGCACAGCATGAGGAGCTGACCTGCTCTTCCATGG
GACCTGCGAGCTGGGCCAGGCCCTCAACGGTGTGTACAGGACCACGGAGGGACGGCTGACAA
AGGCCAGGAACAGCCTGGGTCTCTATGGCCGCACAATAGAACTCCTGGGGCAGGAGGTGACG
CGGGGCGGGATGCGAGCCAGGAACCTTGGGCAAGCCTGTTGGAGACTCAGATGGAGGAGGA
TATTCTGCAGCTGCGAGGCAGAGGCCACAGCTGAGGTGCTGGGGGAGGTGGCCAGGCACAGA
AGGTGCTACGGGACAGCGTGACGCGCTAGAAGTCCAGCTGAGGAGCGCCTGGCTGGGCCCT
GCCTACCGGAGAATTTGAGGTCTTAAAGGCTCACGCTGACAAGCAGAGCCACATCCTATGGGC
CCTCAGAGCCACGTGCGAGCGGCAGAGCGGGAGATGGTGGCACAGCAGCATCGGCTGCGAC
AGATCCAGGAGAGACTCCACACAGCGGCGTCCCAGCCTGAATCTGCCTGGATGGAAC TGAG
GACCAATCATGCTGCAAGGAACACTTCCACGCCCCGTGAGGCCCTGTG CAGGAGGAGCTG
CCTGTTCACTGGGATCAGCCAGGGCGCGGGGCCCCACTTCTGAGCACAGGCAGAGACAGAC
CGAGGCGGGGACAAAGGCAGAGGATGTAGCCCCATTGGGGAGGGGTGGAGGAGGACATGTA
CCCTTTTATGCTACACACCCCTCATTAAAGCAGAGTCTGGCATTTCAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 286

MPVPALCLLWALAMVTRPASAAPMGGPELAQHEELTL LFHGT LQLGQALNGVYRTTEGRLTK
ARNSLGLYGRTIELLGQEVSRGRDAAQELRASLLETQMEEDILQLQAEATAEVLGEVAQAQK
VLRDSVQRLEVQLRSAWLGPAYREFEVLKAHADKQSHILWALTGHVQRQRREMVAQQHRLRQ
IQERLHTAALPA

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GGCAACATGCGCTCAGCAGGCTTGCCCCAGAGCCATTGGCAAAGAATGGACTTGTAAATTTGCAT
CCTGGTGATCACCTTACTCTGGACCAGACCACCAGCCACACATCCAGATTAAAAGCCAGGA
AGCACAGCAAACGTCGAGTGAGAGACAAGGATGGAGATCTGAAGACTCAAATTGAAAAGCTC
TGGACAGAAGTCAATGCCTTGAAGGAAATTAAGCCCTGCAGACAGTCTGTCTCCGAGGCAC
TAAAGTTCACAAGAAATGCTACCTTGTCTCAGAAGGTTTGAAGCATTTCCATGAGGCCAATG
AAGACTGCATTTCCAAGGAGGAATCCTGTTATCCCCAGGAATCCGACGAAATCAACGC
CTCCAAGACTATGGTAAAAGGAGCCTGCCAGGTGTCAATGACTTTTGGCTGGGCATCAATGA
CATGGTCACGGAAGGCAAGTTTGTGTACGCTAACGGAATCGCTATCTCCTTCTCAACTGGG
ACCGTGCACAGCCTAACGGTGGCAAGCGAGAAAATGTGTCTGTTCTCCCAATCAGCTCAG
GGCAAGTGGAGTGATGAGGCCCTGTCGACGAGCAAGAGATACATATGCGAGTTACCATCCC
TAAATAGGCTCTTTCTCCAATGTGTCTCCAAGCAAGATTCATCATAACTTATAGGTTTCATGA
TCTCTAAGATCAAGTAAAAATCATAATTTTTACTTTATAAAAAATTGCAACACAAGATCAAT
GTCCATAGCAATATGATAGCATCAGCCAAATTTGCTAACACATTCCTTTGGGATTTTGCCTT
TCTTGGGGTATAGGGGATCAGAAATATTGATCCTGTGCACGCAAGATAAAATGGCTTCTGCT
AAACAGACATAAATCTTCTCTCTAGTCTTTCTCAGTTGTACAAACCCAGTTTGTTTTCAA
AATCAGACTAGCAATGCAACTCATCACTCTAGAAAAGCAAGCTTAGGCTACCTGAAAGATT
TTCCTTGGAAAGTTAGCGTATGTTTGACTAACAAAAATTCCTACATCAGAGACTCTAGGT
GCTATATAATCCAAAACTTTTCAGCCTGTTGCTCATTCTGTCCATGCTGGCAATAATACC
TTGTGAGCCCATACCCTTATTTGAATTGCTCCATCTCCTGGTGGGACTTGTATCTTGTCT
GCCATATCAGAACACAAACCCCTGAAGAGGTTCTGATTTGATTTTTTTTTTTCTTCATGCC
TACCCTTTTTTGGAAAGTTCCAGCCGCAATTTGAAATGAAATGACAAGGTGTATATTTGAT
CAATTTTCATTCCCACCATTGCATTACAACCTCTAACTTAAATGGGTAAACCTAAGGCATAT
CAAAGAAGCAGATTGCATGATAAACGGAATAGAAAAAAGAACCTACATTTATTTTGCTTT
AGCATCCTTACTCTCACCTTTTATGAGATTGAGAGTGGACTTACATTTCTTTTTTACATTT
TCGTATATTTATTTTTTTTAGCCATCATTATATGTTTAAAGTCTATTATGGGCAACCAATCTT
TGGAAAGCTGAAAATGAATTTAAAGAATGCTATCTTGGAAAATTGCATACGCTGTGCAATT
TTTTATTCTGCCTAGTGTCTATTCTGCTTGTTAACTAGATTGTACAAAATAACTTCATTGCT
TAATATCAAAATTACAAGTTTAGACTTGGAGGGAATGGGCTTTTGAAGAACAAATTTT
AAATATATTTTGTCTTCAAATAAATAGTGTTTAAACATTGAATGTGTTTGTGCAACAATAT
CCCATTTTGCAACTTTAATCATACATGCTTGGAAATTAGTTTTAGCTGTTTTTCATTGCTCA
ATAATTAAGGCTGAATTTCTGATCAATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 288

MAQQACPRAMAKNGLVICILVITLLLDQTTSHTSRLKARKHKKRRVRDKDGLKTQIEKLWT
EVNALKEIQALQTVCLRGTKVHKKCYLASEGLKFHEANEDCISKGGILVIPRNSDEINALQ
DYGKRSLPGVNDFWLGINDMVTEGKFVDVNGIAISFLNWDRAQPNGGKRENCVLFSQSAQGK
WSDEACRSSKRYICEFTIPK

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FIGURE 290

MKLAALLGLCVALSCSSAAAFVLVGSAPVAPVAALESAAEAGAGTLANPLGTINPLKLLS
SLGIPVNHLEGSQKCVaelGPQAVGAVKALKALLGALTVFG

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TGAAGGACTTTTCCAGSACCCCAAGGCCACACCTGGAAGTCTTCGAGCTGAAGGGAGGCACT
CCTTGGCCTCCGCGACCGCATCAGCTGAAGAGGGTGGTGCCCAAGTCTCTGCTCTCCGCTCCTCCTG
GCACAGGTGTGGTGGTGTACCGGCTTGGCCCGAGTCCTCAGTCGCGACAGACCCGACGCCCC
TCGACGACGAGCAGGAGCGGGTATGTGACGGTCTCCGAGGGAGGAAGAGGAATGAGCAGGAGG
CCAGCGAGGAGACCGCCGGTGAGGAAGAGAAGAGCTGGCTGATGCCACGAGGCAGCAGCTT
GCCAAGGAGACTTCAAACCTCGGAATTCAGCCTGCTGCGAAAGATCTCCATGAGGCACGATG
CAACATGGTCTTCTCTCCATTTGGGATGTCTTGGCCATGACAGGCTTGATGCTGGGGGCGA
CAGGGCGCACTGAACCCAGATCAAGAGAGGGCTCCACTGCAGGCCCTGAAGCCCAACGAG
CCCGGGCTCCTGCCTTCTCTTTAAGGGACTCAGAGAGACCCCTCTCCCGCAGCTTGGAACT
GGGCCCTCTCACGAGGGAGTTTGGCTCTCTCCACAGGATTTTGATGTCAAAGAGCTTTCT
TCAATTTATCCAAAGAGTATTTGTATACAGAGTGCCTGCCATGAATTTTCGAATGCCTCA
CAGGCCCAAAGGCTCATGAATCATTACATCAACAAAGAGCTCGGGGGAAAAATCCCCAACT
GTTTGATGAGTAATTAATCTGAACCAAAATTAATTCTTGATATACATCTGTTTCAAAAGGA
AATGGTTGACCCCAATTGACCCTGTCTTACCAGGAGTCGACACTTTCACCTGGACAAGTAC
AAGACAATAAGGTCGCCATGATGTACGCTGACGGTCGAGCGAAGTTTGCCTCCACCTTTGACAAGAA
TTTTCTGGTTGCTGTCTCAAACCTGCCATGCCATCAAGAAATGCCACCATGCTGGTGCTCTCA
TGGAGAAAATGGGTGACCACTCTGCCCTTGAAGACTCATGACCACAGACTTTCGGTGGAGACA
TGGCTCAGAAACATGAAACACCAAAACATGGAAGTTTCTTCCGAAGTTCAAGCTAGATCA
GAGTATGAGATGCATGAGCTGCTTAGGCAGATGGGAATCAGAAGAAATCTTCTCACCCCTTG
CTAGCCTTAGTGAACTCTCAGCTATCTGGAAGAAATCTCCAAGTATCAGGTTGCTTGCAGGA
ACAGTGATTGAAGTTGATGAAGAGGGCAGTGAAGCAGTGGCAGGAATCTTGTCAAGAAATTAC
TGCTTATTCATGCTCTCTGTCTCAAGTGGACCGCCATTTCATTTCATGATCTATGAGA
AAACCTCGGAAATGCTTCTGTTTCTGGGCGAGGTGGTGAATCCGACTCTCTTAATTAAG
ACATGCATAGAACCTCTGCTGCTGTAGTAGAGTCTGAACTGAGGTATCAACACACACAGGA
TACAGCAATGGATGGCAGGGGAGATGTTCCTTTGTTTCTTAACATAGTTTATGGGTGTTCTC
AATAAATAATCAGTAGTCCCCTATCTGTGAGGGGATACATTCAAAGACCCCGACAGATGC
CTGAACCGGTGGACAGTGTCTGAACCTTATATATATTTTTTCTTACACATACATACCTATGAT
AAAGTTTAAATTTATAAATAGGCCAGTAGAAGAGATTAACAAATATAACAACTAAGTAAAA
TGAGTTACTTGAACGCAAGCACTGCAATAGCAATACAGCTCAAACGATATTATAGAGAGGCTA
CTAAGTCTCATGTGGCGAGGAGCATAGACAGTGTGGAGACATTTGGGCAAGGGGAGAAATCA
CTACCTGGGTGGGACAGCAGGACGAGCAGTGAAGATTCACCCACTCATCAGATGGCATGC
TGCTTAAGACTTTTATAGTTTATTCTGGAATTTTCATTTAATGTTTTTGGACCATGGT
TGACATGTGTTACTGAGACTGCGAAGAAGCAAAACCATGGATGAAGGAGGACTACTACAAA
GCATTAATTTGATACATATTTTTTAAAAAATAAAAAAAAAAAAAA

FIGURE 292

MKVVP S L L S V L L A Q V W L V P G L A P S P Q S P E T P A P Q N Q T S R V V Q A P R E E E E D E Q E A S E E K A G E
E E K A W L M A S R Q Q L A K E T S N F G F S L L R K I S M R H D G N M V F S P F G M S L A M T G L M L G A T G P T E T Q I
K R G L H L Q A L K P T K P G L L P S L F K G L R E T L S R N L E L G L S Q G S F A F I H K D F D V K E T F F N L S K R Y F
D T E C V P M N F R N A S Q A K R L M N H Y I N K E T R G K I P K L F D E I N P E T K L I L V D Y I L F K G K W L T P F D P
V F T E V D T F H L D K Y K T I K V P M M Y G A G K F A S T F D K N F R C H V L K L P Y Q G N A T M L V V L M E K M G D H L
A L E D Y L T T D L V E T W L R N M K T R N M E V F F P K F K L D Q K Y E M H E L L R Q M G I R R I F S P F A D L S E L S A
T G R N L Q V S R V L R R T V I E V D E R G T E A V A G I L S E I T A Y S M P P V I K V D R P F H F M I Y E E T S G M L L F
L G R V V N P T L L

FIGURE 293

CTGGGATCAGCCACTGCAGCTCCCTGAGCACTCTCTACAGAGACGCGGACCCAGACATGAG
 GAGGCTCCTCCTGGTCACCAGCCTGGTGGTTGTGCTGCTGTGGGAGGCAGGTGCAGTCCCAG
 CACCCAAGGTCCTTATCAAGATGCAAGTCAAACACTGGCCCTCAGAGCAGGACCCAGAGAAG
 GCCTGGGGCGCCCGTGTGGTGGAGCCTCCGGAGAAGGACGACCAGCTGGTGGTGTGTTCCC
 TGTCCAGAAGCCGAAACTCTTGACCACCGAGGAGAAGCCACGAGGTGAGGGCAGGGGCCCCA
 TCCTTCCAGGCACCAAGGCCTGGATGGAGACCGAGGACACCTGGGCCGTGTCTGAGTCCC
 GAGCCCGACCATGACAGCCTGTACCACCCTCCGCCTGAGGAGGACCAGGGCGAGGAGAGGCC
 CCGGTTGTGGGTGATGCCAAATCACCAGGTGCTCCTGGGACCGGAGGAAGACCAAGACCACA
 TCTACCACCCCCAGTAGGGCTCCAGGGGCCATCACTGCCCCGCCCTGTCCCAAGGCCAGG
 CTGTTGGGACTGGGACCTCCCTACCCTGCCCCAGCTAGACAAATAAACCCAGCAGGCAAA
 AAAAAAAAAAAAAA

FIGURE 294

12345678910111213141516171819202122232425262728293031323334353637383940414243444546474849505152535455565758596061626364656667686970717273747576777879808182838485868788899091929394959697989910010110210310410510610710810911011111211311411511611711811912012112212312412512612712812913013113213313413513613713813914014114214314414514614714814915015115215315415515615715815916016116216316416516616716816917017117217317417517617717817918018118218318418518618718818919019119219319419519619719819920020120220320420520620720820921021121221321421521621721821922022122222322422522622722822923023123223323423523623723823924024124224324424524624724824925025125225325425525625725825926026126226326426526626726826927027127227327427527627727827928028128228328428528628728828929029129229329429529629729829930030130230330430530630730830931031131231331431531631731831932032132232332432532632732832933033133233333433533633733833934034134234334434534634734834935035135235335435535635735835936036136236336436536636736836937037137237337437537637737837938038138238338438538638738838939039139239339439539639739839940040140240340440540640740840941041141241341441541641741841942042142242342442542642742842943043143243343443543643743843944044144244344444544644744844945045145245345445545645745845946046146246346446546646746846947047147247347447547647747847948048148248348448548648748848949049149249349449549649749849950050150250350450550650750850951051151251351451551651751851952052152252352452552652752852953053153253353453553653753853954054154254354454554654754854955055155255355455555655755855956056156256356456556656756856957057157257357457557657757857958058158258358458558658758858959059159259359459559659759859960060160260360460560660760860961061161261361461561661761861962062162262362462562662762862963063163263363463563663763863964064164264364464564664764864965065165265365465565665765865966066166266366466566666766866967067167267367467567667767867968068168268368468568668768868969069169269369469569669769869970070170270370470570670770870971071171271371471571671771871972072172272372472572672772872973073173273373473573673773873974074174274374474574674774874975075175275375475575675775875976076176276376476576676776876977077177277377477577677777877978078178278378478578678778878979079179279379479579679779879980080180280380480580680780880981081181281381481581681781881982082182282382482582682782882983083183283383483583683783883984084184284384484584684784884985085185285385485585685785885986086186286386486586686786886987087187287387487587687787887988088188288388488588688788888989089189289389489589689789889990090190290390490590690790890991091191291391491591691791891992092192292392492592692792892993093193293393493593693793893994094194294394494594694794894995095195295395495595695795895996096196296396496596696796896997097197297397497597697797897998098198298398498598698798898999099199299399499599699799899910001001100210031004100510061007100810091010101110121013101410151016101710181019102010211022102310241025102610271028102910301031103210331034103510361037103810391040104110421043104410451046104710481049105010511052105310541055105610571058105910601061106210631064106510661067106810691070107110721073107410751076107710781079108010811082108310841085108610871088108910901091109210931094109510961097109810991100110111021103110411051106110711081109111011111112111311141115111611171118111911201121112211231124112511261127112811291130113111321133113411351136113711381139114011411142114311441145114611471148114911501151115211531154115511561157115811591160116111621163116411651166116711681169117011711172117311741175117611771178117911801181118211831184118511861187118811891190119111921193119411951196119711981199120012011202120312041205120612071208120912101211121212131214121512161217121812191220122112221223122412251226122712281229123012311232123312341235123612371238123912401241124212431244124512461247124812491250125112521253125412551256125712581259126012611262126312641265126612671268126912701271127212731274127512761277127812791280128112821283128412851286128712881289129012911292129312941295129612971298129913

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGGAGTGAAAGAGCTCTCTG
TACCCAAGGAAAGTGCAGCTGAGACTCAGACAAGATTACAATGAACCAACTCAGCTTCTCTG
TGTTTCTCATAGCGACCACCAGAGGATGGAGTACAGATGAGGCTAATACTTACTTCAAGGAA
TGGACCTGTTCTTCGTCTCCATCTCTGCCAGAAGCTGCAAGGAAATCAAAGACGAATGTCC
TAGTGCATTGTATGGCCTGTATTTTCTCCGACTGAGAATGGTGTTATCTACCAGACCTTCT
GTGACATGACCTCTGGGGTGGCGGTGGACCTGGTGCCAGCGTGCATGAGAATGACATG
CGTGGGAAGTGCACGGTGGGCGATCGCTGCTCCAGTCAGCAGGGCAGCAAAGCAGACTACCC
AGAGGGGGACGGCAACTGGGCCAACTACAACACCTTTGGATCTGCAGAGCGGCCACGAGCG
ATGACTACAAGAACCTTGGCTACTACGACATCCAGGCCAAGGACCTGGGCATCTGGCACGTG
CCCAATAAGTCCCCATGCAGCACTGGAGAAACAGCTCCCTGCTGAGGTACCGCACGGACAC
TGGCTTCTCCAGACACTGGGACATAATCTGTTTGGCATCTACCAGAAATATCCAGTGAAT
ATGGAGAAGGAAAGTGTTGGACTGACAACGGCCCGGTGATCCCTGTGGTCTATGATTTTGGC
GACGCCCAGAAAACAGCATCTTATTACTCACCTATGGCCAGCGGGAATTCAGTCGGGGATT
TGTTTCAGTTCAGGGTATTTAATAACGAGAGAGCAGCCAACGCCTTGTGTGCTGGAATGAGG
TCACCGGATGTAACACTGAGCATCATGCATTGGTGAGGAGGATACCTTCAGAGGCCAGT
CCCCAGCAGTGTGGAGATTTTCTGCTTTGATTTGAGTGGAATATGAAGTATGAACTCATGTTGGTTA
CAGCAGACGCCCTGAGATAACTGAGGCAGCTGTGCTTCTATTCTATCGTTGAGAGTTTGTG
GGAGGGAACCCAGACCTCTCTCTCCAAACCATGAGATCCCAAGGATGGAGAACAACCTACCCA
GTAGCTAGAAATGTTAATGGCAGAAGAGAAAAACAATAATCATATTGACTCAAGAAAAAAA

FIGURE 296

MNQLSFLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTEN
GVIYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGSKADYPEGDGNWANYNTFG
SAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTLGHNLFGI
YQKYPVKYGEKGCWTDNGPVI PVVYDFGDAQKTASYYSYPYGQREFTAGFVQFRVFNNERAAN
ALCAGMRVTGCNTEHHHCIGGGYFPEASPOCGDFSGFDWSGYGTHVGYSSSREITEAAVLL
FYR

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FIGURE 297

GCGGAGCCGGCGCCGGCTGCGCAGAGGAGCCGCTCTCGCGCCGCCACCTCGGCTGGGAGCC
CACGAGGCTGCCGCATCTGCCCTCGGAACAATGGGACTCGGCGCGCAGGTGCTTGGGCCG
CGCTGCTCCTGGGACGCTGCAGGTGCTAGCGTGCTGGGGCCGCCCATGAAAGCGCAGCC
ATGGCGGCATCTGCAAACATAGAGAATTCTGGGCTTCACACAACCTCCAGTGCTAACTCAAC
AGAGACTCTCCAACATGTGCCTTCTGACCATACAAAATGAAACTTCCAACAGTACTGTGAAAC
CACCAACTTCAGTTGCCCTCAGACTCCAGTAATACAACGGTCACCACCATGAAACCTACAGCG
GCATCTAATACAACAACACAGGGATGGTCTCAACAATATGACTTCTACCACCTTAAAGTC
TACACCCAAAAACAAGATGTTTACAGAACAACATCTCAGATATCAACATCCAAATGACCG
TAACCCACAATAGTTCAGTGACATCTGCTGCTTACAGTAAACATCAACAACATATGCAT
TCTGAAGCAAGAAGGATCAAAATTGATACTGGGAGCTTTGTTGGTGGTATTGTATTAAC
GCTGGGAGTTTTATCTATTCTTTACATTGGATGCAAAATGTATTACTCAAGAAGAGGCATT
GGTATCGAACCATAGATGAACATGATGCCATCATTAAAGGAAATCCATGGACCAAGGATGGA
ATACAGATTGATGCTGCCCTATCAATTAATTTGGTTTATTAATAGTTTAAACAATATTCT
CTTTTGAATAAGTATAAACAGGCCATGCATATAATGTACAGTGTATTACGTAATATGTA
AAGATTCTTCAAGGTAACAAGGGTTTGGGTTTTGAAATAAACATCTGGATCTTATAGACCGT
TCATACAATGGTTTTAGCAAGTTCATAGTAAGACAAACAGTCCATCTTTTTTTTTTGCT
GGGGTGGGGGCATTGGTCACATATGACCAGTAATTGAAAGACGTCATCACTGAAAGACAGAA
TGCCATCTGGGCATACAAATAAGAAGTTTGTACAGCACTCAGGATTTTGGGTATCTTTGT
AGCTCACATAAAGAACTTCAGTGTCTTTGACAGCTGGATATCTTAATTACTAATGCCACA
CAGAAATTATACAACTCAAACTAGATCTGAAGCATAAATTTAAGAAAAACATCAACATTTTGG
TGCTTTAAACTGTAGTAGTTGGTCTAGAAACAAATACTCC

298/330

FIGURE 298

MGLGARGAWAALLLGTLQVLLALLGAAHESAAMAASANIENSGLPHNSSANSTETLQHVPSDH
TNETSNSTVKPPTSVASDSSNTTVTMTKPTAASNTTTPGMVSTNMTSTTLKSTPKTTSVSQN
TSQISTSTMIVTHNSSVTSAASSVTITTTMHSEAKKGSKFDTGSFVGGIVLTGLVLSILYIG
CKMYYSRRGIRYRTIDEHDAII

298/330

FIGURE 299

CAGCCGGGTGCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCGAGCCGGGAGCCGG
TCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCAGCGATGCGACCCTGTGGGGAGGC
CTTCTTGGCCTTGGCTCCTTGCTCAGCCTGTCTGCTGCGCTTTCCGTGCTGCTGCTGGC
GCAGCTGTGACAGCGCCCAAGAATTTTCAGGATGTGAGATGTAATGTATCTGCCCTCCCT
ATAAAGAAAATTTCTGGGCATATTTATAATAAGACATATCTCAGAAAGATTGTGATTGCCCT
CATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTGTCTACGCTGTGA
ATGCAAAATATGAAGAAAGAAGCTCTGTCAACAATCAAGGTTACCATTTATAATTTATCTCTCCA
TTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGAGCCCATACTGAAGAGG
CGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATATTGGGGATCACCAGCCTTT
TGCAAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGCCAACGTGCTGAACAAGGTAG
AATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGCGAAAGCTGTCTGTCTGACCGG
CATGTTGTCTCAGCTTAATTTGGGAATTGAATTCAGGTGACTAGAAAGAAACACGGCAGACAA
CTGGAAGAACTGACTGCTGGGTTTTGCTGGGTTTCATTTTAATCCTTGTTGATTTACCAACT
GTTGCTGGAAGATTCAAACCTGGAAGCAAAACCTTGCTTGATTTTTTTTTCTTGTTAACGTA
ATAATAGAGACATTTTTAAAGCACACAGCTCAAAGTCAGCCAATAAGTCTTTTCCTATTTG
TGACTTTTACTAATAAAAATAAATCTGCCTGTAAATTATCTTGAAGTCCTTTACCTGGAACA
AGCACTCTCTTTTACCACATAGTTTTAACTTGACTTTCAAGATAATTTTCAGGGTTTTTG
TTGTTGTTGTTTTTTGTTTGTGTTTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTT
AACAACTTTTTCAAGTCACTTTACTAAACAACTTTGTGAAATAGACCTTACCTTCTATTG
TCGAGTTTCATTTATATTTTGAGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTG
ACTTTTGCACGTACTGTATTATCTGGGTATCTGCTGTGCTGCACCTTCATGGTAAACGGGAT
CTAAATAGCCTGGTGGCTTTTCACAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATG
CAATGCATCTAGAACAACTGGCCATTGTCTAGTTTACTCTAAGACTAAACATGACTGTG
GTGTGTGTGGTCTTACTCATCTTCTAGTACCTTTAAGGACAACTCTAAGGACTGTGCACAT
TGCAATAAAGAAATTTTATTTAAACCCAGCCTCCCTGGATTGATATATATACACATTG
TCAGCATTTCCGGTCTGTGGTGTGAGAGGCAGTGTGTTGAGCTCCAATATGTGCAGCTTTGAAC
AGGGCTGGGGTTGTGGTGCCTCTCTGAAAGGTCTAACCATTTATTGGATAACTGCGCTTTT
TCTTCTATGTCTCTTTTGAATGTAAACAATAAAAAATAATTTTGAACATCAA

FIGURE 300

MATLWGGLRLGSLLSLCLALSVLLLAQLSDAAKNFEDVRCKCICPPYKENS
GHYKNIS QKDCDCLHVVEPMPVRGPDVEAYCLRCECKYEERSSVTIKVT
IIYLSILGLLLLYMYLTL VEPILKRRLFGHAQLIQSDDDIGDHQPFANA
HDVLA RSRANVLNKVEYAAQQRWKLQVQEQ RKS VFDRHVLS

124111-0440660

FIGURE 301

GCACCTGCGACCACCGTGAGCAGT**CATG**GCGTACTCCACAGTGCAGAGAGTCGCTCTGGCCTT
CTGGGCTTGCTCTGGCTCTGTCGCTGCTGCTGCCAAGGCCTTCCTGTCCCGCGGAAGCGG
CAGGAGCCGCCGCCGACACCTGAAGGAAAATTGGGCCGATTTCACCTATGATGCATCATCA
CCAGGCACCCTCAGATGGCCAGACTCCTGGGGCTCGTTTCCAGAGGTCTCACCTTGCCGAGG
CATTTGCAAAGGCCAAAGGATCAGGTGGAGGTGCTGGAGGAGGAGGTAGTGGAAGAGGTCTG
ATGGGGCAGATTATTCGAATCTACGGTTTTTGGGATTTTTTTATATATACTGTACATTCTATT
TAAGGTAAGTAGAATCATCCTAATCATATTACATCA**TGA**AAATCTAATATGGCGATAAAAA
TCATTGTCTACATTAAACTTCTTATAGTTCATAAAATTATTTCAAATCCATCATCTCTTTA
AATCCTGCCTCCTCTTCATGAGGTACTTAGGATAGCCATTATTTCAAGTTTCACATAAGAATG
TTTACTCAATGTTTAAGTGTTTTGCCCCAAAATTCACAATAACAAGGCAGAACTAGGACTT
GAACATGGATCTTTTGGTCTTAATCCAGTGAGTGATACAATTCAATGCACTCCCCTGCCA

CGCGCTTCTTTT

FIGURE 302

MAYSTVQRVALASGLVLALSLLLPKAFLSRGKRQEPPTPEGKLGRFPPMMHHHQAPSDGQT
PGARFQRSHLAEAFKAKGSGGGAGGGGSGRGLMGQIIPYVGFIFLYILYILFKVSRILI
ILHQ

009044-1141
10411-040660

FIGURE 303

CGGCTCGAGTGCAGCTGTGGGGAGATTTTCAGTGCATTGCCTCCCCCTGGGTGCTCTTCATCTT
GGATTTGAAAGTTGAGAGCAGC**ATG**TTTTGCCCACCTGAAACTCATCCTGCTGCCAGTGTTAC
TGGATTATTCCTTGGGCTGAATGACTTGAATGTTTCCCGCCTGAGCTAACAGTCCATGTG
GGTGATTGAGCTCTGATGGGATGTGTTTTCCAGAGCAGAGAAGACAAATGTATATTCAAGAT
AGACTGGACTCTGTCAACAGGAGAGCAGCCAAAGGACGAATATGTGCTATACTATTACTCCA
ATCTCAGTGTGCCTATTGGGCGCTTCCAGAACCAGCTACACTTGATGGGGGACATCTTATGC
AATGATGGCTCTCTCCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGAACCTATATCTGTGA
AATCCGCCTCAAAGGGGAGAGCCAGTGTTCAAGAAGGCGTGGTACTGCATGTGCTTCCAG
AGGAGCCCAAAGAGCTCATGGTCCATGTGGGTGGATTGATTGAGATGGGATGTGTTTTCCAG
AGCACAGAAGTGAACACGTGACCAAGGTAGAATGGATATTTTCAGGACGGCGCGCAAAGGA
GGAGATTGTATTTTCGTTACTACCACAACTCAGGATGTCTGTGGAGTACTCCAGAGCTGGG
GCCACTTCCAGAATCGTGTGAACCTGGTGGGGACATTTTCCGCAATGACGGTTCATCATG
CTTCAAGGAGTGAGGGAGTCAGATGGAGGAACTACACCTGCAGTATCCACCTAGGGAACCT
GGTGTTCAAGAAAACCATTTGTGCTGCATGTCAGCCCGAAGAGCCTCGAACACTGGTGACCC
CGGCAGCCCTGAGGCCTCTGGTCTTGGTGGTAAATCAGTTGGTGATCATTGTGGGAATTGTC
TGTGCCACAATCCTGCTGCTCCCTGTTCTGATATTGATCGTGAAGAAGACCTGTGGAATAA
GAGTTCAGTGAATTCTACAGTCTTGGTGAAGAACACGAAGAAGACTAATCCAGAGATAAAAG
AAAAACCTGCCATTTTGAAAGATGTGAAGGGGAGAAACACATTTACTCCCCAATAATTGTA
CGGGAGGTGATCGAGGAAGAAGAACCAAGTGAAAAATCAGAGGCCACCTACATGACCATGCA
CCAGTTTGGCCTTCTCTGAGGTGAGATCGGAACAACCTCACTTGAaaaaaaAGTCAGGTGGGG
GAATGCCAAAAACACAGCAAGCCTTT**TGA**GAAGAATGGAGAGTCCCTTCATCTCAGCAGCGG
TGAGACTCTCTCCTGTGTGTGTCCTGGGCCACTCTACCAGTGATTTCAGACTCCCGCTCTC
CCAGCTGTCTCCTGTCTCATTGTTTGGTCAATACACTGAAGATGGAGAATTGGAGCCTGG
CAGAGAGACTGGACAGCTCTGGAGGAACAGGCCCTGCTGAGGGGAGGGGAGCATGGACTTGGC
CTCTGGAGTGGGACACTGGCCCTGGGAACCAGGCTGAGCTGAGTGGCCTCAAACCCCGCTT
GGATCAGACCCTCCTGTGGGCAGGGTCTTAGTGGATGAGTTACTGGGAAGAATCAGAGATA
AAAACCAACCCAAATCAA

MFCPLKLILLPVLLDYSLGLNDLNVSPPELTVHVGDSSALMGCVFQSTEDKCFIKIDWTLSPG
EHAKEYVLYYYNLSVPIGRFQNRVHLMGDILCNDGSSLLQDVQEADQGTYICEIRLKGES
QVFKKAVLVHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEIIVFRYY
HKLRMSVEYSQSWGHFQNRVNLVGDIFRNDGSI MLQGVRES DGGNYTCSIHLGNLVFKKTI V
LHVSPEEPRTLVT PAALRPLVLGGNQLV IIVGIVCATILLPV LILVKKTCGNKSSVNSTV
LVKNTKKTNP EIKEKPCHFERCEGEKHIYSPIIVREVIEEEEPSEKSEATYMTMHPVWPSLR
SDRNNLSLEKSGGGMPK TQQA F

CTATGAAGAAGCTTCCTGGAAAAAATAAGCAAAGGAAAAACAATGTGTCCTCATCTCACATG
GTTCTACCTACTAAAGACAGGAAGATCATAAAGTACAGATACTGAAATGTAGAGTTGG
AAACTACATTTTGCAGGTCATTGAAGTCTGAGTCTAGTTCAGTACTCGGGAAGCCATGCA
GGATGAAGATGGATACATCACCTTAAATATTTAAAGTCTGGAAGACAGTCTCTGCTCCGTTG
GCCCTGCATCTCTCTCTGGTGGCGTGTGATGGCTTTGATTCTGCTGATCTGTGCGTGGGG
ATGGTTGTGCGGCTGGTGGCTCTGGGGATTGGTCTGTGATGCGCAATTACCTACAGA
TGAGAATGAAATCGCACAGGAACCTGCAACAATTAGCAAAGCGCTTCTGTCAATATGTGG
TAAAAACAATCAGAACTAAAGGACCTTTCAAAGGTCATAAATGCAGCCCCTGTGACACAAAC
TGGAGATATTATGGAGATAGCTGCTATGGGTTCTTCAGGCACAACTTAACATGGGAAGAGAG
TAAGCAGTACTGCACTGACATGAATGCTACTCTCTGAAAGATTGACAACCGGAACATTGTGG
AGTACATCAAAGCCAGGACTCATTTAATTCGTTGGGTCGGATTATCTCGCCAGAAAGTCGAAT
GAGGTCCTGGAAGTGGGAGGATGGCTCGGTTATCTCAGAAAATATGTTGAGTTTTGGAAGA
TGGAAAAGGAAATATGAATGTGCTTATTTTATAATGGGAAATGACCCCTACCTCTCTGTG
AGAACAAACATTTATTAATGTGTGAGAGGAAGGTGGCATGACCAAGGTGGACCAACTAGCT
TAATGCAAAAGAGGTGGACAGGATAACACAGATAAGGGCTTTATGTGACAATAAAGATATGT
ATGAATGCATCAGTAGCTGAAAAA

FIGURE 306

MQDEDEGYITLNIKTRKPALVSVGPASSSWWRVMAILILLILCVGMVVGLVALGIWSVMQRNYL
QDENENRTGTLQQLAKRFCQYVVKQSELKGTFKGHKCSPCDTNWRYYGDSYGFRRHNLWE
ESKQYCTDMNATLLKIDNRNIVEYIKARTHLIRWVGLSRQKSNEVWKWEDGSVISENMFEEFL
EDGKGNMNCAYFHNGKMHPTFCENKHYLMCERKAGMTKVDQLP

0990440-11401

FIGURE 307

CCACACGCTCCGCGCAGTTCGCGCAGTTCTGCCTCCGCTGCCAGTCTCGCCCGCATCCCGC
CCCGGGGTGTGGCGTCGACTCCGACCCAGGCAGCCAGCAGCCCGCGGGAGCCGGACCGC
CGCCGGAGGAGCTCGGACGCGATGCTGAGCCCCCTCCTTTGTGTAAGCCCGAGTGCGGAGAA
GCCCGGGCAAAACGAGGCTAAGGAGACCAAAGCGGCGAAGTGCAGAGACAGCGGACAAGCAG
CGGAGGAGAAGGAGGAGGAGGCCAACCCAGAGAGGGGCGACAAAAGAAGCGGTGGTGGTGGG
CGTCTGTGGCCATGCGCGCGGCTATCGCCAGCTCGCTCATCCGTCAGAAGAGGCAAGCCCGCG
AGCGCGAGAAATCCAACGCCGTGCAAGTGTGTGACGAGCCCCAGCAAAAGCAAGACAGCTGC
GACAAAAACAAGTTAAATGCTCTTTTCCGGGTCAAACCTCTCGGCTCCAAGAAGGGCGCAG
AAGAAGCCAGCAGCTCAGTTTAAAGGTATAGTTACCAAGCTATACAGCCGACAGGCTTACC
ACTTCAGCTGCAGGCCGATGGAACCAATTGATGCGACCAAGAATGAGGACAGCACTTACACT
CTGTTTAACCTCATCCCTGTGGGTCTGCGAGTGGTGGCTATCCAAGGAGTTCAAACCAAGCT
GTACTTTGGCAATGAACAGTGAGGGATACTTGTACACCTCGGAACCTTTTACACCTGAGTGCA
AATTCAAAGAATCAGTGTTTGAAAATTATTATGTGACATATTATCATATGATATACCGTCAG
CAGCAGTCAGGCCGAGGGTGGTATCTGGGTCTGAACAAAGAAGGAGAGATCATGAAGGCCAA
CCATGTGAAGAAGAACAGCCTGCAGCTCATTTTCTGCCTAAAGCACTGAAAGTGCCCATGT
ACAAGGAGCCATCACTGCACGATCTCACGGAGTTCTCCGATCTGGAAGCGGGACCCCAACC
AAGAGCAGAAGTGCTCTGTGGCGTGCTGAACGGAGGCCAAATCCATGAGCCACAATGAATCAAC
GTAGCCAGTGAGGGCAAAAAGGGCTGTGAACAGAACCTTACCTCCAGTGCTGTTGTAAT
TCTTCTAGCAGCTCTTCAACCAAAAGTCTCAAAATTTGTCAGTGACATTTACCAACAACAACGAG
CAGAGTTCACATCTCTATCTGCCAATAGACCTTCTTATCATCCATACATAAAGC

FIGURE 308

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></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA28498
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><subunit 1 of 1, 245 aa, 1 stop
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><MW: 27564, pI: 10.18, NX(S/T): 1

MAAAIASSLIQRKQRAEREREKSNACKCVSSPSKGKTSCKDNKLVNFSRVKLFSGSKRRRRRP
EPQLKGIVTKLYSRQGYHLQLQADGTIDGTKDEDDSTYTLFNLIPVGLRVVAIQGVQTKLYLA
MNSEGILYLTSELTPECKFKESVFENIYVYSSMIYRQQSGRGWYGLNKEGEIMKGNHVK
KNKPAAHFLPKPLKVAMYKEPSLHDLTEFSRSGSGTPTKRSVSGVLNGGKSMHNEST

N-glycosylation site.

amino acids 242-246

Glycosaminoglycan attachment site.

amino acids 165-169, 218-222

Tyrosine kinase phosphorylation site.

amino acids 93-100

N-myristoylation site.

amino acids 87-93, 231-237

ATP/GTP-binding site motif A (P-loop).

amino acids 231-239

HBGF/FGF family proteins

amino acids 78-94, 102-153

FIGURE 309

CCAGGATGGAGCTGGGGCCTGTATAGCCATATTATTGTTCTATGCTACTAGACATGGGGGGG
 ACTTGGTGAAAAAGGTATTATCCAGCCAGAGGCTCTGGGAGCCCTGTCTTACTGAACCTGGG
 CAACCTGGATATTCTGAGACATATTTGGGGGGATTTCAGTGAAAAAAGTGGGGGATCCCTT
 CCATTTAGAGTGTAGCAAAGGAAAAAACACCAAGGTTGGGTTCTTCTGACATTGGCAGTG
 CCCCAGTAGGGGTGGGATGAGCGAATATTTCCCAAAGCTAAAGTCCCACACCCTGTAGATTAC
 AAGAGTGGATTTGGCAGGAGTGTGCCCAAAATACAGTGGAAAGTGCCTGAAGATATTTAA
 ACCACGTCTTGAAAATTTAGTGGGTCTTGGCTTTGGGATAGGTGAAGTGAAGACAGACACTG
 GAGAGGAGGGAAAGGGGACGTTTTCAATAGGAGGCAAACTCGAGGTTGGGATCCACTGAGG
 AGTACATAGGCTGCTGGATCTGGTGGAGCCAGCACTGGGCCACGGGTGGTAAGTGGCTGCT
 GTGGAGGGGGGTACGTGAGGGGGGGGTCTGGGGCTTATCCTCAGGTCTCTGTGGGTGGGGCAG
 CGAGTCGGGGCCTGAGCGTCAAGAGCATGCCCTAGTGAGCGGGCTCCTCTGGGGGAGCCAG
 CGCGCTCCGGGCGCTGCCGGTTTGGGGGTGTCTCCTCCCGGGGCGCTATGCGCGCGCTGGC
 CAGTAGCCTGATCCGGCAGAAGCGGGAGGTCCGCGAGCCCGGGGCGAGCCGGCCGGTGTGCG
 CGCAGCGGCGCGTGTGTCCCCGCGGCACCAAGTCCCTTTGCCAGAAGCAGCTCCTCATCTGT
 CTGTCCAAGTGCGACTGTGCGGGGGGCGGCCCGCGCGGCGGACCGCGGCCCGGAGCCTCA
 GCTCAAAGGCATCGTCACCAAACTGTTCTGCCGCCAGGGTTTCTACCTCCAGGCGAATCCCG
 ACGGAAGCATCCAGGGCACCCAGAGGATACCAGCTCCTTACCCACTTCAACCTGATCCCT
 GTGGGCCTCCGTGTGGTCACCATCCAGAGCGCCAAGCTGGGTCACTACATGGCCATGAATGC
 TGAGGGACTGCTCTACAGTTGCGCCGATTTCACAGCTGAGTGTGCTTTAAGGAGTGTGTCT
 TTGAGAATTACTACGTCTGTACGCCCTCTGCTCTCTACCGCCAGCGTCGTTCTGTGCGGGGCC
 TGGTACCTCGGCCTGGACAAGGAGGGCCAGGTCATGAAGGAAAACCGAGTTAAGAAGACCAA
 GGCAGCTGCCCACTTTCTGCCCAAGCTCCTGGAGGTGGCCATGTACCAGGAGCCTTCTCTCC
 ACAGTGTCCCGAGGGCTCCCTTCCAGTCCCCCTGCCCTCGAATGTAGTCCCTGGACTG
 GAGGTTCCCTGCACTCCAGTGAGCCAGCCACCACCACAACCTGT

FIGURE 310

MAALASSLIRQKREVRPEGGSRPVSAQRRVCPRGTSKLCQKQLLILLISKVRLCGGRPAPDR
GPEPQLKGIIVTKLFCRQGFYLANPDGSIQGTPEDTSSFTFNLPVGLRVVTIQSAKLGHY
MAMNAEGLLYSSPHFTAECRFKECVFENYYVLYASALYRQRSSRAWYLGLDKEGQVMKGNR
VKKTKAAAHFLPKLLEVAMYQEPSLSHVSPEASPPSPAP

Tyrosine kinase phosphorylation site:

amino acids 199-207

N-myristoylation sites:

amino acids 54-60, 89-95, 131-137

HBGF/FGF family signature:

amino acids 131-155

FIGURE 311

ATGGCCGCGGCCATCGCTAGCGGCTTGATCCGCCAGAAGCGGCAGGCGCGGGAGCAGCACTG
GGACCGGCCGCTCTGCCAGCAGGAGGCGGAGCAGCCCCAGCAAGAACC GCGGCTCTGCAACG
GCAACCTGGTGGATATCTTCTCCAAAGTGCGCATCTTCGGCCTCAAGAAGCGCAGGTTGCGG
CGCCAAGATCCCCAGCTCAAGGGTATAGTGACCAGGTTATATTGCAGGCAAGGCTACTACTT
GCAAAATGCACCCCGATGGAGCTCTCGATGGAACCAAGGATGACAGCACTAATTCTACACTCT
TCAACCTCATACCAGTGGGACTACGTGTTGTTGCCATCCAGGAGTGAAAACAGGGTTGTAT
ATAGCCATGAATGGAGAAGGTTACCTCTACCCATCAGAACTTTTACCCCTGAATGCAAGTT
TAAAGAATCTGTTTTTGAAAATTATTATGTAATCTACTCATCCATGTTGTACAGACAACAGG
AATCTGGTAGAGCCTGGTTTTTGGGATTAAATAAGGAAGGGCAAGCTATGAAAGGGAAACAGA
GTAAAGAAAACCAACCAGCAGCTCATTTTCTACCCAAGCCATTGGAAGTTGCCATGTACCG
AGAACCATCTTTGCATGATGTTGGGGAAACGGTCCCGAAGCCTGGGGTGACGCCAAGTAAAA
GCACAAGTGCCTCTGCAATAATGAATGGAGGCAACCAAGTCAACAAGAGTAAGACAACATAG

CGGCTCTGCAACG

FIGURE 312

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA28503

><subunit 1 of 1, 247 aa, 1 stop

><MW: 27702, pI: 10.36, NX(S/T): 2

MAAAIASGLIRQKRQAREQHWDPRPSASRRSSPSKNRGLCNGNLVDIFSKVRI FGLKKRRLR
RQDPQLKGIVTRLYCRQGYLQMHPDGDGTDKDDSTNSTLFNLI PVGLRVVAIQGVKTGLY
IAMNGEGYLYPSELF TPECKFKESVFENYYVIYSSMLYRQQESGRAWFLGLNKEGQAMKGNR
VKKTKPAAHFLPKPLEVAMYREPSLHDVGETVPKPGVTPSKSTSASAIMNGGKPVNKS KTT

N-glycosylation site.

amino acids 100-104, 242-246

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 28-32, 29-33

Tyrosine kinase phosphorylation site.

amino acids 199-207

N-myristoylation site.

amino acids 38-44, 89-95, 118-124, 122-128, 222-228

HBCF/FGF family proteins.

amino acids 104-155, 171-198

FIGURE 313

GGGGAGAGGAATTGACCATTGAAAAGGAGACTTTTTTTTTTGGTGGTGGTGCTGTTGGGTGCTTGCAAAAAAT
GAAGGATGCAGGACGCAGCTTTCTCCTGGAACCGAACGCAATGGATAAACTGATTGTGCAAGAGAGAAGGAAGA
ACGAAGCTTTTTCTGTGAGCCCTGGATCTTAACA CAAATGTGTATATGTGCACACAGGGAGCATTCAAGAATG
AAATAAACCAAGAGTTAGACCCGCGGGGTTGGTGTGTTCTGACATAAATAAATAATCTTAAGCAGCTGTTCCC
CTCCCCACCCCAAAAAAAGGATGATTGGAATGAAGAACCAGGAGTTCACAAAGAAAAAGTATGTTCAATTT
TTCCTCTATAAAGGAGAAAGTGAGCCCAAGGAGATATTTTGGAAATGAAAAGTTTGGGGCTTTTTAGTAAAGTAA
AGAAGCTGGTGGTGGTGGTCTTTCTTTCTTTTGAATTTCCCAAGAGGAGAGGAATTAATAATACATCTGC
AAAGAAATTTGAGAGAAAGAAAGTTGACCGCGGCAGATTGAGGCATTGATTGGGGGAGAGAAACCGAGAGCA
CAGTTGGATTGTGCCTATGTTGACTAAAAATGACGGATAATTGCAGTTGGATTTTTCTTCATCAACCTCCTTT
TTTTTAAATTTTTATTCTCTTTGGTATCAAGATCATGCGTTTTCTTTGCTTCTTAACCACCTGGATTTCCATCT
GGATGTTGCTGTGATCAGTCTGAAATACAACCTGTTGAATTCAGAAGGACCAACACCGATAAAATATGAATG
TTGAACAAGATGACCTTACATCCACAGCAGATATGATAGTCTAGGTTTAAACAGGGCCCTATTGACCCCT
GCTTGGTGGTGGTGGTCTTCAACTTCTTGTGGTGGTGGTCTGGTGGGGCTCAGACCTGCCCTTCTGTGT
GCTCTGCAGAACAGTTGACGAAGTGATTGTGTTGCGAAAAACCTGCGTGAGGTTCCGGATGGCATCTCC
ACCAACACACGGCTGCTGAACCTCCATGAGAACCAGATCCAGATCATCAAAGTGAACAGCTTCAAGCACTTGAG
GCACTTGGAAATCCTACAGTTGAGTAGGAACCATATCAGAACCATTGAAATGGGGCTTTCAATGGTCTGGCGA
ACCTCAACACTCTGGAACCTCTTGACAATCGTCTTACTACCATCCCGAATGGAGCTTTGTATACTTGTCTAAA
CTGAAGGAGCTCTGTTGCGAACAACCCCATTTGAAAGCATCCCTTCTTATGCTTTTAAACAGAATTCCTTCTTT
GCGCGCTAGACTTAGGGGAATTGAAAAGACTTTTACATCATCAGAAGTGCCCTTGAAGGTCTGTCCAACT
TGAGTATTTGAACCTTGCCATGTGCAACCTTCGGGAAATCCCTAACCTCACACCGCTCATAAAACATAGATGAG
CTGGATCTTTCTGGGAATCATTTATCTGCCATCAGGCCTGGCTCTTCCAGGGTTGATGCACCTTCAAAAAC
GTGGATGATACAGTCCAGATTCAAGTGATTGAACGGAATGCCTTTGACAACCTTCAGTCACTAGTGAGATCA
ACCTGGCACACAATAATCTAACATTACTGCCTCATGACCTCTTCACTCCCTTGATCATCTAGAGCGGATCAT
TTACATCAACACCTTGAACCTGTAACCTGTGACATACTGTGGCTCAGCTGGTGGATAAAGACATGGCCCCCTC
GAACACAGCTTGTGTGCGCCGGTGAACACTCCTCCCAATCTAAGGGGAGGTACATTGGAGAGCTCGACCAGA
ATTACTTCACATGCTATGCTCCGTGATTGTGGAGCCCTCGACAGCTCAATGTCACTGAAGGCATGGCAGCT
GAGCTGAAATGTGCGGCTCCACATCCCTGACATCTGTATCTTGGATTACTCCAAATGGAACAGTCATGACACA
TGGGCGCTACAAAGTGCGGATAGCTGTGCTCAGTGATGGTACGTTAAATTTACAAATGTAACCTGTGCGAAGATA
CAGGCATGTACATGATGTGTGAGTAATTCGTTGGGAATACTACTGCTTCAGCCACCTGAAATGTTACTGCA
GCAACCACTACTCCTTTCTTACTTTTCAACCGTCACAGTAGAGACTATGGAACCGCTCAGGATGAGGCAAG
GACCACAGATAACAATGTGGGTCCACTCCAGTGGTGCAGTGGGAGACCAACCAATGTGACCACCTCTCTCACAC
CACAGAGCACAAAGTCGACAGAGAAAACCTTCAACATCCAGTGACTGATATAAACAGTGGGATCCAGGAAT
GATGAGGTGATGAAGACTACCAAAATCATCATTTGGGTGTTTGTGGCCATCACACTCATGGCTGCAGTGTGCT
GGTCACTTTTCTACAAGATGAGGAAGCAGCACCATCGGCAAAACCATCACGCCCCAACAGGACTGTTGAAATTA
TTAATGTGGATGATGAGATTACGGGAGACACACCATGGAAGGCCACTGCCATGCTGCTATCGAGCATGAG
CACCTAAATCACTATAACTCATACAATCTCCCTTCAACCAACACAACAACAGTTAACACAATAAATCAATACA
CAGTTTCAGTGCATGAACCGTTATTGATCCGAATGAACCTAAAGACAAATGTACAAGAGACTCAAATCTAAACAA
TTTACAGAGTTTACAAAACCAACAAATCAAAAAAAGACAGTTTATTAAAAATGACACAATGACTGGGCTAA
ATCTACTGTTTCAAAAAGTGTCTTTACAAAAAACAAGAAAGAAATTTATTATTAAAAATCTATTG
TGATCTAAAGCAGCAAAAA

FIGURE 314

MLNKMTLHPQQIMIGPRFNALFDPLLVLALLQLLVVAGLVRAQTCPSVSCSNQFSKVIC
 VRKNLREVPDGIStNTRLNLHENQIQIIVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA
 NLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS
 YISEGAFEGLSNRLYNLAMCNLREIPNLTPLIKLDLDELDSGNHLSAIRPGSFQGLMHLQKL
 WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLLHNPWNCNDIL
 WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAE
 LKCRASLTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQDTGMYTCMVNSVGN
 TTASATLNVTAATTTFFSYFSTVTVETMEPSQDEARTTDNNVGPTPVVDWETTNVTTSLTPQ
 STRSTEKTFITPVDINSIGIPGIDEVMKTKIIIGCFVAITLMAAVMLVIFYKMRKQHRQN
 HHAPTRTVEIINVDDEITGDTPMESHLMPAIEHEHLNHYSYKSPFNHTTTVNTINSIHSS
 VHEPLLIRMNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419,
 434-438, 442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
 391-397, 422-428, 433-439, 531-537

GCGCCGGGAGGCCCATCTGCCCCAGGGGCACAGGGCGCGGGGCCGGCTCCCGCCCGGCACAT
GGCTTGCAGCCACCTCTGGCGGCACCCAGCGAGCGCGCCAGCTCGCCCGAGGTCGCTCGGA
GGCGCCGGCGCGCCGGAGCCCAAGCAGCAACTGACGGGGGAAGCGCCGCGCTCGGGGATC
GGCATGTCCTCTCTCTCTCTCTCTGCTAGTTTCTCTACTATGTGTTGAACCTTGGGGACTCA
CACTTGAGATCAAGAGAGTGGCAGAGGAAAGGTCACTTTGCCCTGCCACCATCACTGGGG
TTCAGAAAAAGACACTCTGGATATTGAATGGCTGCTCACCGATAATGAAGGAACCAAAAA
GTGGTGATCACTTACTCCAGTCGTCACTGTCTACAATACTTGACTGAGGAACAGAGGCGCG
AGTGGCTTTTGGCTTCCAAATTCTGGCAGAGAGTGCCTCTTGAGATTGAACCTCTGAAGC
CCAGTGATGAGGGCCGGTACACCTGTAAGGTTAAGAATTACGGGCGCTACGTGTGGAGCCAT
GTCACTTTAAAAGCTCTTAGTGAGACATCAAGTCCCAAGTGTGAGTTGGAAGGAGAGCTGAC
AGAAGGAAGTGAAGTCACTTGTGAGTGTGAGTCACTCTCGGCACAGAGCCCATGTGTATT
ACTGCGACGGAATCCGAGAGAAGAGGGTACAGATGAAGCTCTGCTCTCCCAATCTAGGATT
GACTACCAACCCCTGGACGAGTCTGTGCTGAGGAATCTTACCATTGCTCTACTCTGAGCTGTA
CCAGTGCACAGCAGGCACGAAAGCTTGGGAAGGAAAGCTGTGTGGTGGCAGTAACGTGTACAGT
ATGTACAAGCACTCGGCATGTTGTCAGGACAGCTGTCAGCAGCATAGTGCTGGAGCCCTGCTG
ATTTCTCTCTTGGTGTGGCTGCTAATTCCGAAGGAAGAACAAGATAGTATGAGGAAGA
GAGACCTAATGAAATTCGAGAAGATGCTGAAGCTCCAAAGCCCGTCTTGTGAAACCCAGCT
CCTCTTCTCTGAGCTCTGGAGCTCAAGCTCAAGCTTGTGTTCTTCTCTCACTCGCTCCACAGAAAT
AGTGCTCAAGCAGCCAGCGGACACTGTCAACTCAGCAGCAACCCAGCGAGGCTGGCCAC
CCAGGCATGACAGCCTAGTGGGGCCAGAGTGTGAGAGTTTCTGACCAAAAGAAAGTCCACCAT
CTAATCTGACAAAGCAGAAACCAACCCAGCATGATCCCCGACGAGCAGGCTTCCAA
ACGGTTGAATTACAATGGACTTGACTCCACGCTTTCCTAGGAGTCAGGGTCTTTGGACTC
TTCTCGTCACTTGAGCTCAAGTCAACGACGACCAACAGCATGAGAGGTCATCTAAGTAGCA
GTGAGCATTGACGGAACGATTCAGATGACATTTTCTTATACATAACCAACAGCAAA
AGGATGTAAGCTGATTTCATCTGTAAAAGGCATCTTATTGTGCTTTAGACCAGAGTAAGGG
AAAGCAGGAGTCCAAATCTATTTTGTGACCAGGACCTGTGGTGAGAAGTTGGGGAAGGTG
AGGTGAATATACCTAAAATTTTAATGTGGGATATTTGTATCAGTGGCTTGATTCACAAAT
TTCAAGAGGAATGGGATGCTGTTGTAAATTTTCAATGCAATTTCTGCAAACTTATGGATT
ATTAGTATTACAGAGTCAGCAGCAACCAACGACCTTATACACTTCTACACACTGTAC
TGAGCTAACCACTTCTAAGAACTCCAAAAAGGAAACATGTGTCTTCTATTCTGACTTAAC
TCTATTGTGATCAAGTTTGGATATTAATTTCAAGGGGATGAAATAGTGGGAGTGGGA
AGAGTGAATGAGTTTCTCCACTCTATACTAATCTGCAATTTGTATTGAGCCCAAAATAC
TATGAAAGGAGACAAAAATTTGTGACAAAGGATTGTGGAAGAGTTTCCACTCTCTATGATGTT
ATGAGGATTTGTGACAAACATTGACAATAATATGGAAGCAATTGTGGATTTCCTCTCAAT
CAGATGCCTCAAGGACTTTCTCGCTAGATATTTCTGGGAAGGAGAAATACAACATGTCAAT
TATCAACGTCCTTAGAAGAAATTTCTGACAGAAAGGAGTCTAGGAATGCTGAAGAGTTA
CCCAACATACCAATATAGTCTCTCTTCTTGAGAAAAATGGAACAGAAATGCAAGACTGG
GTGGACTAGAAAGGGAGATTAGATCAGTTTTCTCTTAATATGTCAGGAAGGTAGCCGGCA
TGGTGCCAGGCACCTGTAGGAAATCCAGCAGGTGGAGGTGCAGTGAGCCGAGATTATGCC
ATTGCACTCCAGCTGGGTGACAGAGCGGACTCCGCTCT

FIGURE 316

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419
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><subunit 1 of 1, 373 aa, 1 stop
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><MW: 41281, pI: 8.33, NX(S/T): 3

MSLLLLLLLLVSYVGLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTPDNEGKQKV
VITYSSRHYNNLTTEEQKGRVAFASNFLAGDASIQIEPKPSDEGRYCKVKNSGRYVWSHV
ILKVLVRPSKPKCELEGELETGSDTLQCESSSGTEPIVYVYQRIEKEGEDERLPPKSRID
YNHPGRVLLQNLTSYSGLYPCTAGNEAGKESCVVRVTVQVYQSIGMAGAVTIGAVALLI
FLRWLLIRRKDKERYEEERENIREDAEAPKARLVKPSSSSGSRKSSGSSSTRSTANS
ASRSTLTSDAAPGLTAQYSLVPEDEAPKRVGSEPKKVHHANLTKAETTPSMIPSQSRFQTV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 232-251

FIGURE 317

CGCGAGGCGCGGGGAGCCTGGGACCAGGAGCGAGAGCCGCCTACCTGCAGCCGCCGCCACGGCAGCGCAGCCA
 CCATGCGCGCTCCTGCTGTGCTTCTGCTCCTGTGCGGAGTAGTGGATTTCGCCAGAAAGTTTGGATATCACTACT
 CCTGAAGAGATGATTGAAAAAGCCAAAGGGGAAACTGCCATCTGCCATGCAAAATTTACGCTTTAGCTCCCGAAGA
 CCAGGAGCCGCTGGACATCCAGTGGCTGATATCACAGCTGATAATCAGAAGGTGGATCAAGTGATTATTTAT
 ATCTCGAGACAAAAATTTATGATGACTACTACTCCAGATCTGAAAGGCCGAGTACATTTTACGAGTAATGATCTC
 AAATCTGGTGATGCATCAATAATGTAAACGATTTACAACCTGTCAGATATTGGCACATATCAGTGCAAGAGTGA
 AAAAGCTCCTGCTGTTGCAAAATAAGAAATTCATCTGCTGGTAGTCTTGTTAAGCCTTCAGGTGCGAGATGTTACG
 TTGATGGATCTGAAGAAATTTGGAAGTGACTTTAAGATAAAATGTGAACCAAAAGAGGTTCACTTCCATTACAG
 TATGATGGCAGAAAATTTGCTGACTCACAGAAAATGCCCACTTCATGTTTACGAGAAATGACTTCATCTGTTAT
 ATCTGTAAAAAATGCCCTCTCTGAGTACTCTGGACATACAGCTGTACAGTCAGAAAACAGAGTGGGCTCTGATC
 AGTGCCCTGTTGGCTCTAAACGTTGTCCTCCTTCAATAAAGCTGGACTAATTGCAGGAGCCATTATAGGAAC
 TTGCTTGCTCTAGCGCTCATTTGGTCTTATCATCTTTGCTGCTGATAAAAAGCGCAGAGAGAAAAATATGAAA
 GGAAGTTTATCACGATATCAGGGAAGATGTGCCACCTCCAAAGAGCCGATACGTCCTACCTGCCAGAGCTACATCG
 GCAGTAATCATTATCCTCGGGCTCCATGTCTCCTTCCAACATGGAAGGATATCCAAAGACTCAGTATAACCAA
 GTACCAAGTGAAGACTTTGAACGCACCTCTCAGAGTCCGACTCTCCCACTGCTAAGTTCAAGTACCTTACAA
 GACTGATGGAATTACAGTTGTATTAATATGGACTACTGAAGATCTGAAGTATTGATTATTTGACTTTATTTT
 AGGCCTCTAGTAAAGACTTTAAATGTTTTTAAAAAAGCACAAGGCACAGAGATTAGCAGCTGTAAGAACAC
 ATCTACTTTATGCAATGGCATTTAGACATGAAGTCAGATGTCATGTCAAAATTAGTACGAGCCAATTCCTTGT
 TAAAAAACCTATGTATAGTACACTGATAGTTAAAGATGTTTTATTATATTTCAATAACTACCACATAACAA
 ATTTTTAACTTTTATATGCATATCTGATATGTGGTCTTTTAGGAAAAGTATGGTAAATAGTTGATTTTCAA
 AGGAAATTTTAAATTTCTACGTTCTGTTAATGTTTTGCTATTTAGTTAAATACATTGAAGGGAAATACCCG
 TCTTTTCCCTTTTATGCACACAACAGAAAACAGCGTTGTCTGCGCTCAAACTATTTTTATTGGCACTACA
 TGATTTACACAATTTCTTAAACAACGACATAAAATAGATTTCTTGTATATAAATAACTTACATACGCTCCA
 TAAAGTAAATTTCAAAGGTGCTAGAACAATCGTCCAGTTCTACAGTGTCTCGTATCCAACAGAGTTGATGC
 ACAATATATAAATACTCAAGTCCAATATTAABAACTTAGGCACCTTGACTAATTTAATAAAATTTCTCAAAC
 TATCAATATCTAAAGTGCATATATTTTTAAGAAAGATTATTTCAATAACTTCTATAAAAAATAAGTTTGATGG
 TTTGGCCCATCTAACTTCACTACTATTTAGTAAGAACTTTAACTTTTAAATGTGTAGTAAGGTTTATCTACCTT
 TTTCTCAACATGACACCAACCAATCAAAACGAAGTTAGTGAGGTGCTAAACATGTGAGGATTAAATCCAGTGAT
 TCCCGTCACAATGCAATTCAGAGGAGGAGTACCATGTCTAGTGGATTGGGCGATATGGTTATTTTTCTTCCC
 TGATTTGGATAACCAAATGGAACAGGAGGAGTATGATTCTGATGGCCATTCCCTCGATACATTCTCTGGCTT
 TTTTCTGGGCAAGGCTGCCACATTTGGAAGAGGTGGAATATAAGTTCTGAATCTGTAGGGAAGAGAACAT
 TAAGTTAATTCAGAGAAAAAATCATCATCTATGTTCCAGATTTCTCATTAAGACAAAGTTACCCACAACAT
 GAGATCAGATCATAGTGACACTCCTATTGTCAGGTCTAAATACATTAACAACTCATGTAAATAGGCGGTATAA
 GTTATAACAGGTGACCAATGTTTTCTGAATGCATAAAGAAATGAATAAATCAACACAGTACTTCCGTAACAA
 CTTCAACCAAAAAAGCCCAAAACATGGAAACGAATGGAAGCTTTGAAGGACATGCTTGTTTAGTCCAGTGGCTT
 CCACAGCTGGCTAAGCCAGGAGTCACTTGGAGGCTTTTAAATACAAACACTTTGAGAGTACTTCCGTAACCT
 AGCAAACTAATGCAGAAACAGAAAACTCACTACCGCATGTCTCACITATAAGTGGAGGTATGATGAAGAACT
 TATGAACACAAAGGAAGAAACATAGACATTTGGAGTCTAATTTGAGAGGGGAGGCTGGGAGAGGAAAGAGCA
 GAAAGATAAATCTTGAATGCTGCCITCACACCTGGGTGATGAATAATATGTACACCAAAATCCCTGTGCACAC
 TGTTTACCTATGGAACAAACCTTCATGTGATCCCTAAACCTAAATAAAGTTAAAAAAGGAAAAA
 AAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAA
 AAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAA

FIGURE 318

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA82361

><subunit 1 of 1, 352 aa, 1 stop

><MW: 38938, pI: 7.86, NX(S/T): 3

MALLLCFVLLCGVDFARSLSITTPPEEMIEKAKGETAYLPCKFTLSPEDQGPLDIEWLISPA
DNQKVDQVIILYSGDKIYDDYYPDLKGRVHFTSNDLKSGDASINVTLQLSDIGTYQCKVKK
APGVANKKIHLVVLVKPGARCYVDGSEEIGSDFKIKCEPKEGSLPLQYEWQKLSDSQKMPT
SWLAEMTSSVISVKNASSEYSGTYSCTVRNRVGSQCLLRNLNVVPPSNKAGLIAGAIIGTLL
ALALIGLIIFCCRKKRREEKYEKEVHHDIREVDVPPPKSRTSTARSYIGSNHSSLGSMSPSNM
EGYSKTQYNQVPSEDFERTPQSPTLPPAKFKYPYKTDGITVV

Signal sequence.

amino acids 1-19

Transmembrane domain:

amino acids 236-257

N-glycosylation sites.

amino acids 106-110, 201-205, 298-302

Tyrosine kinase phosphorylation sites.

amino acids 31-39, 78-85, 262-270

N-myristoylation sites.

amino acids 116-122, 208-214, 219-225, 237-243, 241-247,
245-251, 296-302

Myelin P0 protein.

amino acids 96-125

FIGURE 319

TGAAATGACTTCCACGGCTGGGACGGGAACCTTCCACCCACAGTATGCCTCTGATTGGTGA
ATGGTGAAAGGTGCCTGTCTAACTTTTCTGTAAAAAGAACAGCTGCCTCCAGGCAGCCAGCC
CTCAAGCATCACTTACAGGACCAGAGGGACAAGACATGACTGTGATGAGGAGCTGCTTTTCG
CAATTTAACACCAAGAAGATTGAGGCTGCTTGGGAGGAAGGCCAGGAGGAACACGAGACTG
AGAGATGAATTTTCAACAGAGGCTGCAAAGCCTGTGGACTTTAGCCAGACCCCTTCTGCCCTG
CTTTGCTGGCGACAGCCTTCTCAAATGCAGATGGTGTGTGCTCCCTTGCTGGGTTTTACCTTG
CTTCTCTGAGGCCAGGTATCAGGGGGCCAGGGCCAAGAATTCACCTTTGGGCCCTGCCAAGT
GAAGGGGGTGTGTCCCGAGAAACTGTGGGAAGCCTTCTGGGCTGTGAAAGACACTATGCAAG
CTCAGGATAACATCACGAGTGCCCGGCTGCTGCAGCAGGAGGTTCTGCAGAACGTCCTCGGAT
GCTGAGAGCTGTTACCTTGTCCACACCCCTGCTGGAGTTCTACTTGAAAACGTGTTTCAAAA
CCACCACAATAGAACAGTTGAAGTCAGGACTCTGAAGTCATTCTCTACTCTGGCCCAACACT
TTGTTCTCATCGTGTCACAACTGCAAACCAGTCAAGAAATGAGATGTTTTCCATGCAGAC
AGTGACCAACGGCGGTTTCTGCTATTTCCGGAGAGCTTCAAAAGTGTGGACGTAGAAGCAGC
TGTGACCAAAGCCCTTGGGGAAGTGACATTCTTCTGACCTGGATGCAGAAATTTCTACAAGC
TCTGAATGTCTAGACCAGGACCTCCCTCCCCTGGCACTGGTGTGTTCCCTGTGTCATTTCA
AACAGCTCTCCCTTCTATGCTGTTCACTGGACATTCACGCCCTTGCCATGGGTCCCATTCT
TTGGCCCAGGATTATTGTCAAAGAAGTCATTCTTTAAGCAGCGCCAGTGACAGTCAGGGAAG
GTGCCTCTGGATGCTGTGAAGAGTCTACAGAGAAGATTCTGTATTATTACAACCTCTATTT
AATTAATGTCAGTATTTCAACTGAAGTCTATTTATTTGTGAGACTGTAAGTTACATGAAG
CAGCAGAATATTGTGCCCATGCTTCTTTACCCCTCACAACTCCTTGCCACAGTGTGGGGCAG
TGGATGGGTGCTTAGTAAGTACTTAATAAAGTGTGGTGCTTTTTTGGCCTGTCTTTGGATT
GTTAAAAAACAGAGAGGGATGCTTGGATGTAAAAGTGAACCTCAGAGCATGAAAATCACACT
GTCCTTCTGATATCTGCAGGGACAGAGCATTGGGGTGGGGGTAAGGTGCATCTGTTTGAAAG
TAAACGATAAAATGTGGATTAAAGTGCCAGCACAAAGCAGATCCTCAATAAACATTTCATT
TCCCACCCACACTCGCAGCTCACCCCATCATCCCTTCCCTTGGTGCCCTCCTTTTTTTTT
TATCTTAGTCATTCTTCCCTAATCTTCCACTTGAGTGTCAAGCTGACCTTGTCTGATGGTGAC
ATTGCACCTGGATGTACTTCAATCTGTGATGACATCCCTGCTAATAAAGACACATAA
CTCCAAAAAAGAAAAAAGAAAAAAGAAAAA

FIGURE 320

MNFQQRQLSWLTARFCPPLLATASQMQMVVLPCLGFTLLWSQVSGAQGEFHFGPCQVK
 GVPVQKLWEAFWAVKDTMQAQDNITSARLLQQEVLQNVSDAESCYLHTLLEFYLKTVFKNH
 HNRTEVVRTLKSFSTLANNFVLIVSQLQPSQENEMFSIRDSAHRRFLLFRFAFKQLDVEAAL
 TKALGEVDILLTWMQKFYKL

amino acids 1-42

amino acids 85-89, 99-103, 126-130

FIGURE 321

AAGGAGCAGCCCGCAAGCACCAAGTGAGAGGC**ATGA**AGTTACAGTGTGTTTCCCTTTGGCTC
CTGGGTACAATACTGATATTGTGCTCAGTAGACAACCACGGTCTCAGGAGATGTCTGATTTT
CACAGACATGCACCATATAGAAGAGAGTTTCCAAGAAATCAAAAGAGCCATCCAAGCTAAGG
ACACCTTCCCAAATGTCACTATCCTGTCCACATTGGAGACTGTGCAGATCATTAAGCCCTTA
GATGTGTGCTGCGTGACCAAGAACCTCCTGGCGTTCTACGTGGACAGGGTGTTCAAGGATCA
TCAGGAGCCAAACCCCAAAATCTTGAGAAAAATCAGCAGCATTGCCAACCTCTTCTCTACA
TGCAGAAAACCTGCGGCAATGTCAGGAACAGAGGCAGTGTCACTGCAGGCAGGAAGCCACC
AATGCCACCAGAGTCATCCATGACAACTATGATCAGCTGGAGGTCCACGCTGCTGCCATTAA
ATCCCTGGGAGAGCTCGACGTCTTTCTAGCCTGGATTAAATAAGAATCATGAAGTAATGTTCT
CAGCT**TGA**TGACAAGGAACCTGTATAGTGATCCAGGGATGAACACCCCTGTGCGGTTTACT
GTGGGAGACAGCCACCTTGAAGGGGAAGGAGATGGGGAAGGCCCTTGACAGTGAAAGTCC
CACTGGCTGGCCTCAGGCTGTCTTATTCGCTTGAAAATAGGCAAAAGTCTACTGTGGTAT
TTGTAATAAACTCTATCTGCTGAAAGGGCCTGCAGGCCATCCTGGGAGTAAAGGGCTGCCTT
CCCATCTAATTTATTGTAAAGTCATATAGTCCATGTCTGTGATGTGAGCCAAGTGATATCCT
GTAGTACACATTGTACTGAGTGGTTTTTCTGAATAAATTCATATTTTACCTATGA

FIGURE 322

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92282
><subunit 1 of 1, 177 aa, 1 stop
><MW: 20452, pI: 8.00, NX(S/T): 2
MKLQCVSLWLLGTILILCSVDNHGLRRCLISTDMHHIEESFQEIKRAIQAKDTFPNVITILST
LETIQIIKPLDVCCVTKNLLAFYVDRVFKDHQEPNPKILRKISSIANSFLYMQKTLRQCQEQ
RQCHCRQEATNATRVIHNDYDQLEVHAAAIKSLGELDVFLAWINKNHEVMFSA

Signal sequence:

amino acids 1-18

N-glycosylation sites.

amino acids 56-60, 135-139

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 102-106

N-myristoylation site.

amino acids 24-30

Actinin-type actin-binding domain signature 1.

amino acids 159-169

FIGURE 323

CCCGTGCCAAAGAGTGACGTAAGTACCGCCTATAGAGTCTATAGGCCACTTGGCTTCGTTAG
AACGCGGCTACAATTAATACATAACCTTATGTATCATACACATACGATTTAGGTGACACTAT
AGAATAACATCCACTTTGCTTTCTCTCCACAGGTGTCCACTCCCAGGTCCAACCTGCACCTC
GGTTCTATCGATAATCTCAGCACCAGCCACTCAGAGCAGGGCAGATGTTGGGGGCCGCGCT
CAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGCGTCCTCAGAGCCTATCCCA
ATGCCTCCCCACTGCTCGGCTCCAGTGGGGTGGCCTGATCCACCTGTACACAGCCACAGCC
AGGAACAGCTACCACCTGCAGATCCACAAGAAATGGCCATGTGGATGGCGCACCCCATCAGAC
CATCTACAGTGCCTGTATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGA
TGAGCAGAAGATACCTCTGCATGGATTTCAGAGGCAACATTTTGGATCACACTATTTTCGAC
CCGGAGAAGTGCAGGTTCCAACACCAGACGCTGGAAAACGGGTACGACGCTACCACTCTCC
TCAGTATCACTTCCTGGTCAGTCTGGGCCGGGCGAAGAGAGCCTTCCTGCCAGGCATGAACC
CACCCCCGTACTCCAGTTCTCTGTCCGGAGGAACGAGATCCCCCTAATTCACCTTCAACACC
CCCATACCACGGCGGCACACCCGGAGCCGGAGGACGACTCGGAGCGGGGACCCCTGAACGT
GCTGAAGCCCCGGGCCGAGTAGCCCGCGGCCCTCTGTTCAGAGGAGCTCCCGAGCG
CTGAGGACAACAGCCGATGGCCAGTGACCCATTAGGGGTGGTCAGGGGCGGTGAGTGAAAC
ACGCACGCTGGGGGAACGGGCCCGGAAGGCTGCCGCCCTTCGCCAAGTTTCATCTAGGGTCG
CTGG

FIGURE 324

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA142238

><subunit 1 of 1, 251 aa, 1 stop

><MW: 27954, pI: 9.22, NX(S/T): 1

MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSWGGLIHLYTATARNSYHLQIHKNGHVD
GAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENC RFQHQTLENGY
DVIHSPQYHFLVSLGRAKRAFLPGMNPPPYSQLSRNEIPLIHENTPIPRRHTRSAEDDSE
RDPLNLVKPRARMTFAPASCSQELPSAEDNSPMASDPLGVVRGGRVNT HAGGTGPEGCRPFA
KFI

Important features of the protein:

Signal peptide:

amino acids 1-24

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 175-179

N-myristoylation site.

amino acids 33-39, 100-106, 225-231, 229-235

HBGF/FGF family proteins

amino acids 73-124

GGAAAGGTTACCCGAGAGACAGCCAGCAGTTCCTGTGGAGCAGCGGTGGCCGGCTAGGATG
GGCTGTCTCTGGGGTCTGGCTCTGCCCTTTTCTTCTTCTGTGGGAGGTGGGGTCTCTGG
GAGCTCTGCAGGCCCCAGCACCCGCAGAGCAGACACTGCGATGACAACGGACGACACAGAAG
TGCCCGCTATGACTCTAGCACCGGGCCACGCCGCTCTGGAACCTCAAACGCTGAGCGCTGAG
ACCTCTTCTAGGGCCTCAACCCAGCCGGCCCCATTCCAGAAGCAGAGACCAGGGGAGGCCAA
GAGAAATTTCCCTGCAAGAGAGACCAGGAGTTTCAAAAACATCTCCAACTTCATGTTGC
TGATCGCCACCTCCGTGGAGACATCAGCCGCCAGTGGCAGCCCCGAGGGAGCTGGAATGACC
ACAGTTCAGACCATCACAGGCAGTGATCCCAGGAAGCCATCTTTGACACCTTTGCACCGA
TGACAGCTCTGAAGAGGCAAAGACACTCACAAATGGACATATTGACATTGGCTCACACCTCCA
CAGAAAGCTAAGGGCCTGTCTCAGAGAGCAGTGCTCTTCCGACGGCCCCCATCCAGTCATC
ACCCCGTCAACGGGCTCAGAGAGCAGCGCTCTTCCGACGGCCCCCATCCAGTCATCACCCC
GTCACGGGCTCAGAGAGCAGCGCTCTTCCGACGGCCCCCATCCAGTCATCACCCCCTCAT
GGTCCCCGGGATCTGATGTCTACTCTCTCGTGAAGCCCTGGTGACTGTCAAAACATCGAG
GTTATTAATTGCAGCATCAGAAATAGAAACAACAACTTCCAGCATCTCCCTGGGGCTCAGA
CATAGATCTCATCCCTCAGGAAGGGGTGAAGGCCCTCGTCCACTCCGATCCGACACCGCTGTGC
CTGACTCCACTGAAGCAAACACACATCACTGAGGTCAAGCCTCTGCCGAGACCTGTCC
ACAGCCGGCACACAGAGTCAGCTGCACCTCATGCCAGGTTGGGACCCCACTCCCACTAA
CAGCGCCACAGAAAGAGAGTGACAGCACCCGGGGCCACGACCTCAGTGGAGCTCTGGTCA
CAGTTAGCAGGAATCCCTTGAAGAAACCTCAGCCCTCTCTGTTGAGACCAAGTTACGTC
AAAGTCTCAGGAGCAGCTCCGGTCTCCATAGAGGCTGGGTGACAGTGGGCAAAACAACCTC
CTTTGCTGGGAGCTCTGCTTCTCTTACAGCCCTCGGAAGCCGCCCTCAAGAACTTCAACC
CTTCAGAGACACCGACCATGGACATCGCAACCAAGGGGCCCTTCCCAACAGCAGGGACCT
CTTCCTTCTGTCCCTCCGACTACAACCAACAGCAGCCGAGGGACGAACAGCACCTTAGCCAA
GATCACAACTCAGCGAAGACCAGATGAAGCCCCAACAGCCACGCCACGACTGCCCGGAC
GAGGCCGACCCACAGACCTGAGTGTCAGGTGAAATGGAGGTTCTCTCTCTCGCGCTGAGTG
TGGCTTCCCCGGAAGACCTCACTGACCCAGAGTGGCAGAAAGGCTGATGCAGCAGCTCCAC
CGGGAACCTCACGCCCACGCGCTCACTTCCAGGTCTCCTTACTGCGTGTGACGAGAGGCTA
ACGGACATCAGCTGCAGCCAGGCATGTCCCGTATGCCAAAGAGGGTGCTGCCCCTAGCCTG
GGCCCCACCGACAGACTGCAGCTGCGTTACTGTGCTGAGAGGTACCCAGAAGGTTCCCATG
AAGGGCAGCATGTCCAAGCCCCAATCCCAAGATGTGGCAACAGGACCTCGTTCATCATCCAC
CGGAGTGATGTATGGGGAGGGGCTTCACTGTTCCCAAGAGTGTCCTTGGACTCACCTGG
CATAGTCTCTGTGTTTCAGTAAGAGAGACCTGATCACCCATCTGTGTGTTCCATCTCTGCA
TTAAATTCATCAGTGTGGCCCAAAAAA

FIGURE 326

MGCLWGLALPLFFFCWEVGVSGSSAGPSTRRADTAMTTDDTEVPAMTLPAGHAALETQTL
 ETSSRASTPAGPIPEAETRGAKRISPAETRSFTKTSNFMVLIATSVETSAASGSPEGAGM
 TTVQTITGSDPEEAI FDTLCTDSDSEEAKTLTMDILT LAHTSTEAKGLSSESSASSDGPHPV
 ITPSRASESSASSDGPHPVITPSRASESSASSDGPHPVITPSWSPGSDVTL LAEALVTVTNI
 EVINC SITEIETTSSIPGASDIDLIPTEGVKASSTSDPPALPDSTEAKPHITEVTASAETL
 STAGTTESAAPHATVGTPLPTNSATEREVTAPGATTL SGALVTVSRNPLEETSALS VETPSY
 VKVSGAAPVSI EAGSAVGKTTSFAGSSASSYSPSEALKNFTPSETPTMDIATKGPFPTSRD
 PLPSVPPTTTNSSRGTNSTLAKITTS AKTTMKPQQPRPRLPGRGRPQT

N-glycosylation sites:

amino acids 252-256, 445-449, 451-455

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 84-90

Casein kinase II phosphorylation sites.

amino acids 37-41, 108-112, 131-135, 133-137, 148-152, 165-169,
 246-250, 254-258, 256-260, 269-273, 283-287, 333-337, 335-339,
 404-408, 414-418, 431-435

N-myristoylation sites.

amino acids 2-8, 19-25, 117-123, 121-127, 232-238, 278-284, 314-
 320, 349-355, 386-392, 397-403, 449-455

ATP/GTP-binding site motif A (P-loop).

amino acids 385-393

FIGURE 327

GCGGAGCATCCGCTGCGGTCTCGCGGAGACCCCGCGGGATTGCGCGGTCTTCCCGCGG
 GCGCGACAGAGCTGTCTCGCACCTGGATGGCAGCAGGGGCGCCGGGGTCTCTCGACGCCA
 GAGAGAAATCTCATCTGTGTCAGCCTTCTTAAAGCAAACCTAAGACCAGAGGGAGGATTAT
 CCTTGACCTTTGAAGACCAAACTAAACTGAAATTTAAATGTTCTTCGGGGGAGAGGGGAG
 CTTGACTTACACTTTTGTAATAATTGTCTCCTGACACTAAGGCTGTCTGTCTAGTCAGAATT
 GCCTCAAAAAGAGTCTAGAAGATGTTGTCTTACATCCAGTCATCTCTTTCTAAGGGAATC
 AGAGGCAATGAGCCCGTATATACTTCAACTCAAGAAGACTGCATTAATTCTTGCTGTTCAC
 AAAAAACATATCAGGGGACAAAGCATGTAACCTTGATGATCTTCGACACTCGAAAAACAGCTA
 GACAACCCAACTGCTACCTATTTTCTGTCCCAACGAGGAAGCCTGTCCATTGAAACACGCA
 AAAGGACTTATGAGTTACAGGATAATTACAGATTTTCCATCTTTGACCAGAAATTTGCCAAG
 CCAAGAGTTACCCAGGAAGATTCTCTCTTACATGGCCAATTTTCACAAGCAGTCACTCCCC
 TAGCCCATCATCACAGATTATTCAAAGCCCGCATATCTCATGGAGAGACACACTTTCT
 CAGAAGTTTGGATCCTCAGATCACCTGGAGAACTATTTAAGATGGATGAAGCAAGTGCCCA
 GCTCCTTGCTTATAAGGAAAAAGGCCATTCTCAGAGTTCACAATTTTCTCTGATCAAGAAA
 TAGTCTATCTGCTGCCTGAAATGTGAGTGCCTCCAGCTACGGTGGCAGTTGCTTCTCCA
 CATACCACCTCGGCTACTCCAAGGCCCGCCACCTTTCTACCACCAATGCTTCAGTGACACC
 TTCTGGGACTTCCAGCCACAGCTGCCACCACAGCTCCAGCTGAACCACTGTCACTTTCT
 AGCCTCCACGACCTTATTCTACAGTTTTTACACGGGCTGCGGCTACACTCCAAGCAATG
 GCTACAACAGCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGA
 AACCATACCGTTTTACAGAAATCTCCAACCTTAACTTTTGAACACAGGGAATGTGTATAACCTA
 CTGCACTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAACTGCTTCTCGGGAAGGT
 AGGGAGGCCAGTCCAGGCAGTTCTCCCAGGGCAGTGTCCAGAAATCAGTACGGCCTTCC
 ATTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCTGTTCTCGGTGATAGGCC
 TCGTCTCTCGGGTAGAATCCTTTCGGAATCACTCCGCAGGAAACGTTACTCAAGACTGGAT
 TATTGTATCAATGGGATCTATGTGGACATCTAAGGATGGAACCTCGTGTCTCTTAATTCATT
 TAGTAACCCAGAAGCCCAATGCAATGAGTTTCTGCTGACTTGCTAGTCTTAGCAGGAGGTTG
 TATTTTGAAGACAGGAAATGCCCTTCTGCTTCTCTTTTTTTTTTTGGAGACAGAGTCTT
 GCTCTGTGCCCAGGCTGGAGTGCAGTAGCACGATCTCGGCTCTCACCACCACTCCGTCTC
 CTGGGTTCAAGCGATTCTCCTGCCTCAGCTCCTAAGTATCTGGGATTACAGGCATGTGCCA
 CCACACCTGGGTGATTTTGTATTTTGTAGTAGACGGGGTTTACCATTGTTGGTCAGGCTG
 GTCTCAAACCTCTGACCTAGTGATCCACCTCTCGGCCTCCCAAGTGCTGGGATTACAGG
 CATGAGCCACCAAGCTGGCCCCCTTCTGTTTTATGTTTGGTTTTTGAAGAAGGAATGAAGTG
 GGAACCAATTAGTAATTTTGGTAACTGTCTCTAAATATTAGCTAAAAACAAGCTCT
 ATGTAAGTAATAAAGTATAATTGCCATATAAATTTCAAATTTCAACTGGCTTTTATGCAAA
 GAAACAGGTAGGACATCTAGGTTCCAATTCATTACATTTCTGGTTCAGATAAATCAAC
 GTTTATATCAATTTCTAATGGATTGCTTTTCTTTTATATGGATTCTTTAAAACTTATT
 CCAGATGTAGTTCCTTCCAATTAATATTGTAATAATCTTTTGTACTCAA

FIGURE 328

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410
 ><subunit 1 of 1, 431 aa, 1 stop
 ><MW: 46810, pI: 6.45, NX(S/T): 6
 MFFGGEGSLTYTLVIICFLTLRLSASQNCCLKKSLDVDVIDIQSSLSKGIRGNEPVYTSTQED
 CINSCCSTKNISGDKACNLMI F DTRKTARQPN CYLFFCPNEEACPLKPAKGLMSYRIITDFP
 SLTRNLPSQELPQEDSL LHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSDHLEKLF
 KMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSATPKPATLL
 PTNASVTPSGTSQPQLATTAPPVTTVTSTQPPTTLISTVFTRAAATLQAMATTAVLTTFQAP
 TDSKGSLETIPFTEISNLT LNTGNVYNPTALSM SNVESSTMNKTASWEGREASPGSSSQGSV
 PENQYGLPFEKWLLIGSLLFGVLFVLVIGLVLLGRILSESLRRKRYSR LDYLINGIYVDI

Signal sequence.

amino acids 1-25

Transmembrane domain.

amino acids 384-405

N-glycosylation sites.

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 415-419

Tyrosine kinase phosphorylation site.

amino acids 50-57

N-myristoylation sites.

amino acids 4-10, 48-54, 315-321

FIGURE 329

TCCTCCACGGTGTCCAGAGGCCAGAA**ATC**CGGCTCTGGTCTGCTATGGGGTGGCTGCTGCT
CCCAGGGTTATGAAGCCCTGGAGGGCCAGAGGAAATCAGCGGGTTCGAAGGGGACATGGTGT
CCCTGCGAGTGCACCTACAGGGAAGAGTCAGGAGCCACCGGAAGTACTGTTGTCAGGAAGTGT
GGGATCCTCTCTCTGCTGCTCTGGCACCTCTATGCAGAAGAAGAAGGCCAGGAGACAAT
GAAGGGCAGGGGTGCTCATCCGTGCACGCCCGAGGAGCTCTGCTCATTTGTACCTCTGTGGA
ACCTCACCTGCAAGACGCTGGGAGTACTGGTGTGGGGTCGAAAAACGGGGGCCGATAGT
TCTTTACTGATCTCTCTGTTGCTCTTCCAGGACCTTGCTGTCTCTCTCTCTCTCCAC
CTTCGAGCCTCTGGCTACAACAGCCTGCAGCCCAAGGCAAAAGCTCAGAAAACTCCAGCCCT
CAGGATTGACTTCTCTCGGGCTCTACCCGCGACCCACCAAGCAGGACGGGGAAGACAGGG
GCTGAGGCCCTCCATTGCCAGGGAATCCCACTACGGGCAGAAAGGACTTCTCAGTATAC
AGGAACCTCTCTCCACCCAGCGACTCTCTCTCTGCGAGGAGCTCCCGCCCCCATGCAGC
TGGACTCCACCTCAGCAGAGACACCACTGCTCAGCTCTCAGCAGTGGCAGCTCTAAGCCGAG
GTGTCCATCCGATGGTCCGCATCTGGCCCCAGTCTGTGGTGTCTGAGCCTTCTGTGCAGC
CGCAGGCTGTAGTCGCTTCTGCAGCCACCTGCTCTGTGGAGAAGGAAGCTCAACAGGCCA
CGGACAGCAGAGGAACGAGAAGTTCTGGCTCTCAGCTTGACTGCGGAGGAAAAAGGAAGCC
CCTTCCAGGCCCTCAGGGGGGAGCTGTATCTCGATGCTCCCTCCACACATCTGAGGAGAGA
CTGGGGCTCTCGAAGTTTGTCTCAGCG**TAGG**GGCAGGAGCCCTCTGCGCGAGCCAGCA
GAAGCAGTATGGCTGGCTGGATCAGCACCGATTCCCGAAAGCTTCCACCTCAGCCTCAGAG
TCCAGCTGCCCGGACTCAGGGGCTCTCCACCCTCCCGAGGCTCTCTCTGTGATGTTCTCA
GCCTGACCTACAGGCGTTTGTGACGCTGGAGCCGAGCGGTGGCCCTTGCTCTTCCGGCTG
GAGACTGGGACATCCCTGATAGGTTACATCCCTGGGCAGATACAGGCTGCTGACCTCA
GCAGGGCCAGACAGGCTCAGTGATGTTGGTCTGAGTTTCAATCTGCCAGGAAGCTCTGGG
TCTATGCCCAGTGTGCGACCGTGCCTTCTCCCACTCAGAGCCCACTTGTCTTCCCTCC
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GGGGTGGAGCTGGGATCTGGCTTCTCTTTGAACCACTGCATCAGCCCTTTCAGGAAGCT
GTAAAAACGATGATCTCTGGCCCCAACAGACCACCAAAACCATCTCTGGGCTTGGTGCAG
GACTCTGAATTTCAACAATGGCCAGTGACTGTGCGATTTGGATTTGAGGGCCAGTGGGGCT
ATGAACGCTCACACCCCTTACGTTAGAGTGTGACCTTAGGTTGAGTGTGATGCTTCACTGCC
CAATAGATCTGCTCTGTCTGCGACACCAGATCCAGTGGGGACTCCCTGAGGCCCTGCTAAG
TCCAGGCCCTTGGTAGGTGACATTCAGGATTCAGAGTAAGCCGAGGACCCAGACAGATGG
TGGCTTTNCAATTGGCCCTCCTGNCNATGCTCTTGTGCTTTGAAAAAATGATGAAGA
AAACCTTGGCTCTTCTTGTCTGGAAGGGTTACTTGCTATGGGTCTGCTGGCTCAGAGA
GAAAGTAGAGAAAAACAGAGTGACAGTAGTCTTAACACAGAGGAGTAGGAACAGGCGCG
ATACCTGAAGGTTGACTCCGATCCAGCCCTGGAGAGGGGTGGGGGGTGGTGAAGTA
GCACAACCTACTATTTTTTCTTTTTCCATATATTATGTTTTTAAAGACGAATCTCGTGT
GCTGCCACGCTGGAGTGCAGTGGCAGATCGCAACTCCGCTCTCTGGGTCTCAAGTGATT
CTTCTGCTCAGCTCCCGAGTAGCTGGATTACAGGCACGCCACCACACCTGGCTAATT
TTTGTAATTTTATGATAGTGGGTTTACCAATGTGGCCAGCTGGTGTGAACTCTTCGAC
CTCAAAATGAGCTCTGCTGCTTCCCAATTTGCGGGATTCAGGATGAGGCACCTGTG
TCTGGGCCCTATTCTCTTTAAAAAGTGAAATTAAGAGTTGTTCAATGCAAAACTTGGAAAG
ATGAGGAGGAAAAAGAAAGGAAGAAAAAATTCACCCATAGTCTCACCAGAGACTCAT
TATTTGGTTTTGGTTGACTTCTTCCACTCTTTCTCTTCACTAATTTGGCGGTGTTCTT
TTTACAGAGCAATTATCTTGTATACAACCTTTGTATCTGCTCTTTCCACCTTATCGTTC
ATPACTTATTCAGCACTTCTCTGTGTTTTACAGACCTTTTATAAATAAATGTTCTATCA
GCTGCATAAAAAAAAAAAA

FIGURE 330

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196

<subunit 1 of 1, 332 aa, 1 stop

<MW: 36143, pI: 5.89, NX(S/T): 1

MRLLVLLWGCLLLPGYEALEGPEEISGFEGDTVSLQCTYREELRDHRKYWCRKGGILFSRCS
 GTIYAE EEGQETMKGRVSIRD SRQELSLIVTLWNLTLQDAGEYWCVEKRGPD ELLISLFV
 FPGPCCPPSPSPTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQKGTGA EAPPLPG
 TSQYGHERTSQYTGTSHPATSPAPAGSSRPPMQLDSTSAEDTSPALSSGSSKPRVSI PMVRI
 LAPVLVLLSLLSAAGLIAFCSHLLLWRKEAQQATETQRNEKFWLSRLTAE EKEAPSQAPEGD
 VISMPPLHTSEELGFSKFVSA

Important features:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 248-269

N-glycosylation site.

amino acids 96-99

Fibrinogen beta and gamma chains C-terminal domain.

amino acids 104-113

Ig like V-type domain:

amino acids 13-128